

160342

From: Chan, Christina
Sent: Monday, July 25, 2005 2:14 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 10/019071

Please rush. Thanks Chris

-----Original Message-----

From: Davis, Minh-Tam
Sent: Monday, July 25, 2005 2:11 PM
To: Chan, Christina
Subject: Rush search request for 10/019071

Please search in commercial database, issued patent files and PGPUB:
Amino acids 263-793 of SEQ ID NO:3.
Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

CRIFE

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

THIS PAGE BLANK (USPTO)

O'Bryen, Barbara

From: Davis, Minh-Tam
Sent: Monday, July 25, 2005 3:50 PM
To: O'Bryen, Barbara
Subject: RE: problem with search request for 10/019071

Hi Barb,
amino acids 263-793 of Seq Id No **2**, not **3**.
I apologize for the mistake.
Thanks
Tam

-----Original Message-----

From: O'Bryen, Barbara
Sent: Monday, July 25, 2005 3:38 PM
To: Davis, Minh-Tam
Subject: problem with search request for 10/019071
Importance: High

Hi Tam,
You had requested that we search "amino acids 263-793 of Seq Id No 3" from case 10/019071.
Seq ID 3 of this case is a nucleotide sequence, 45 nucleotides long. How would you like to modify your search request?
Please send your response directly to me, and **not** to the STIC-biotech/chemLib mailbox, since I now have the search on my desk.
Thanks,
Barb

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model
Run on: July 25, 2005, 16:54:32 ; Search time 42 Seconds
(without alignments)
1216.455 Million cell updates/sec
Title: US-10-019-071-2_COPY_263_793
Perfect score: 2896
Sequence: 1 DDSLNDCRIIFVDEVKIER.....VNOPLQTLVNLFPFGYGNCR 531
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	600	20.7	641	2 E96612	probable transcript
2	556	19.2	622	2 H96684	probable RING zinc
3	533.5	18.4	598	2 A96685	probable RING zinc
4	473	16.3	650	2 D96612	hypothetical prote
5	427	14.7	461	2 T01825	hypothetical prote
6	353.5	12.2	432	2 T00949	hypothetical prote
7	311.5	10.8	299	2 C75384	conserved hypothet
8	270.5	9.3	794	2 D84765	similar to mammali
9	263	9.1	788	2 C84616	similar to mammali
10	229.5	7.9	650	2 T06648	hypothetical prote
11	226	7.8	651	2 F84743	similar to mammali
12	194.5	6.7	669	2 F96756	hypothetical prote
13	192.5	6.6	954	2 G86312	hypothetical prote
14	170	5.9	4957	2 T03455	ALR protein - huma
15	170	5.9	5262	2 T03454	ALR protein - huma
16	162	5.6	1829	2 T34239	hypothetical prote
17	158	5.5	1280	2 T51500	hypothetical prote
18	157	5.4	811	2 T08738	hypothetical prote
19	153	5.3	1250	2 T00454	hypothetical prote
20	152.5	5.3	202	2 F88469	protein C28H8.9 [i
21	151.5	5.2	1350	2 T42697	hypothetical prote
22	150.5	5.2	728	2 S57142	hypothetical prote
23	150.5	5.2	1787	2 T20160	hypothetical prote
24	148	5.1	312	2 G84472	hypothetical prote
25	147	5.1	1722	1 I78879	retinoblastoma bin
26	146	5.0	429	2 C84640	similar to mammali
27	146	5.0	609	2 A43906	nuclear phosphopro
28	146	5.0	1479	2 T17401	transcription regu
29	143.5	5.0	1518	2 D96660	protein F2K11.14 [

30	139	4.8	449	2 T12495	hypothetical prote
31	138.5	4.8	530	2 I38558	Mi-2 autoantigen 2
32	138	4.8	1560	2 I54361	SMCX protein - hum
33	137.5	4.7	371	2 A53302	probable transcrip
34	137	4.7	1146	2 H96796	hypothetical prote
35	136	4.7	1033	2 I48775	Smcx protein (esca
36	134.5	4.6	796	2 T08555	pathogenesis-relat
37	133	4.6	571	2 T40911	probable PHD-type
38	130.5	4.5	397	2 S26731	neuro-D4 protein -
39	129.5	4.5	564	2 I48776	spematogenesis re
40	129.5	4.5	2561	2 T24864	hypothetical prote
41	129	4.5	1088	2 T14917	homeotic protein P
42	127	4.4	1576	2 S65774	homeotic protein H
43	125.5	4.3	350	2 G01950	hypothetical prote
44	125	4.3	1257	2 T01020	hypothetical prote
45	124.5	4.3	2447	2 T16870	hypothetical prote

ALIGNMENTS

RESULT 1

E96612
Probable transcription factor F12K22.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96612
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96612
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-641 <STO>
A:Cross-references: UNIPROT:Q9FVS3; GB:AE005173; NID:g11079528; PIDN:AAG29238.1; GSPDB:G C:Genetics:
A:Gene: F12K22.14
A:Map position: 1
C:Superfamily: Arabidopsis thaliana probable transcription factor F12K22.14; RING finger

Query Match 20.7%; Score 600; DB 2; Length 641;
Best Local Similarity 26.5%; Pred. No. 6.4e-34;
Matches 172; Conservative 68; Mismatches 160; Indels 248; Gaps 19;
QY 56 CHLCGRDPPKQMLCECDMAFYICLDPLSLVPSSEDEWYCPCECRNDASEVVLG--- 112
Db 15 CWRCKNSPPPEESLTGCGVTPHVSCLSSPPKTLASTLQWCHPCDCSIEIDPLPVGSGAT 74
QY 113 -----ERLESK----- 119

Db 75 GFESAGSLVAAIRAIEADESLSTEKAKMRQLLSGKGVDEEDDEEKKKKKGKPNL 134
QY 120 ----- 119
Db 135 DVLSALGNLMCSFCMQLPERPVTKPCGHNAACLCFKWMQGRKTCCKRSIIPERWAK 194
QY 120 -----KNAKMASATSS-----SORD-----WGKGMACVQRT 145
Db 195 NPRINSSIVAIRLAKVSKSAATTSKVFFHISNQDRPDKAFTTERAKTKCKANAAG-- 252
QY 146 KECTIVPSNHVGPDP-----GIPVGTWFRFVQSVESGVHRPHVAGHGRSDGSY 196
Db 253 KIYVTIPDPHFGPIPAENDPVRNQLLVGSWEDRLCROWGAHFPHPVAGIAGQSTYGAQ 312
QY 197 SLVLAGGVDDVDHGNPFYTYTSGGRDLSGNKRT-AEQSCDQKLTNTNRALALNCFAPIN 255

Db	215	YVTVPDHFGPIPAEHDVPVNRQGVLVGESWENRVECRQGVHLPHVSCIAGQEDYGAQSV	274
QY	199	VLAGGYEDVDHGNFTYTG-SGGRDLSGNKRTAEQSCDKLTNTNRALALNCFAPINDQ	257
Db	275	VISGGYKDDHGEWFLYTGSRGRHFANE-----DQEPEDLNEALRVSC-----	319
QY	258	EGNAEKDWSRGKPVVRVNRVVGKSKKYAPAGNRYDGIYKVVKYWPKEKSGFLWRYL	317
Db	320	-----EMGYFVRVRSYK--DRYSAYAPKEGVRYDGVYRTEKCW---RKARFPVCRYL	367
QY	318	LRRDDDEPGFW-TKEGDKRIKKLGLTMQYPEGVYLEALANRERKENSKEEEOQEGGFA	376
Db	368	FVRCONEPAPWNSDESGDRPRPL---PNPIE--LETASDLFERKESPSWDFDEA----	417
QY	377	SPRTGKGKWKRSAGGSPRAGSPRRTSKK	406
Db	418	----GRWRWK-----PPPANHEQERMK	437
RESULT 6			
T00949			
hypotheical protein T3F12.10 - Arabidopsis thaliana			
C:Species: Arabidopsis thaliana (mouse-ear cress)			
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004			
C:Accession: T00949			
R.; GnoJ., L.; Huang, E.N.; Habermann, K.; Hameed, A.; Hasegawa, A.; Jensen, K.; Schutz, K.			
submitted to the EMBL Data Library, October 1997			
A:Description: Arabidopsis thaliana BAC T3F12 from chromosome IV.			
A:Reference number: Z14210			
A:Accession: T00949			
A:Status: translated from GB/EMBL/DBDJ			
A:Molecule type: DNA			
A:Residues: 1-432 <GNO>			
A:Cross-references: UNIPROT:O22280; EMBL:AC002983; NID:g2443893; PID:g2565009			
C:Genetics:			
A:Map position: 4			
A:Introns: 121/3; 296/2; 329/3; 351/2; 385/3			
A:Note: T3F12.10			
C:Superfamily: Arabidopsis thaliana probable transcription factor F12K22.14; RING finger			
F:105-153/Domain: RING finger homology <RRN>			
Query Match			
Best Local Similarity 12.2%; Score 353.5; DB 2; Length 432;			
Matches 121; Conservative 49; Mismatches 137; Indels 143; Gaps 19;			
QY	1	DDSLNDCRIIFVDEVFKIERPGSGSPMVDNPMRRKSGPSCKHCKDDVNRLCRVCA---CH	57
Db	58	DESMTD-----ADETKKRILSGDCEABE--NNSKDGELASLNDGVDAFTAICEDLNCS	110
QY	58	LCGGRODDPKQLMCDCECDMAFIHYICLDPLPSSVPSEDEW-----YCPECRNDAGEWJIA	111
Db	111	LCNQLPDRPVTILCG-----HNFCL-----KCFDKWIDQGNQICATCRSTIPDKMAA	157
QY	112	GERLRES-----KNAKVASATS-----SSQRDWGKGMACVGRTECTI-----	150
Db	158	NPRVNSLSVIRYRVKAVTAGVTANFFPFTSNQD---GPNAPFTKRAKIGEENAAARI	214
QY	151	---VPSNHYGPIDP-----GIPYGTWRRFVRVQVSESGVHRPHVAGIHGRSNDGSYSL	198
Db	215	YVTVPDHFGPIPAEHDVPVNRQGVLVGESWENRVECRQGVHLPHVSCIAGQEDYGAQSV	274
QY	199	VLAGGYEDVDHGNFTYTGSGGRDLSGNKRTAEQSCDKLTNTNRALALNCFAPINDQ	258
Db	275	VISGGYKDDHGEWFLYTGSRGRHFANE-----DQEPEDLNEALRVSC-----	295
QY	259	GAEAKDWSRGKPVVRVNRVVGKSKKYAPAGNRYDGIYKVVKYWPKEKSGFLWRYL	317
Db	296	-----RSYK-----DRYSAYAPKEGVRYDGVYRTEKMWKARFPFDSFKVCRYL	338
QY	318	LRRDDDEPGFW-TKEGDKRIKKLGLTMQYPEGVYLEALANRERKENSKEEEOQEGGFA	376

Db	339	FVRCONEPAPWNSDESGDRPRPL---PNPIE--LETASDLFERKESPSWDFDEA----	388
QY	377	SPRTGKGKWKRSAGGSPRAGSPRRTSKK	406
Db	389	----GRWRWK-----PPPANHEQERMK	408
RESULT 7			
C75384			
conserved hypothetical protein - Deinococcus radiodurans (strain R1)			
C:Species: Deinococcus radiodurans			
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004			
C:Accession: C75384			
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;			
S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma			
Science 286, 1571-1577, 1999			
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.			
A:Reference number: A75250; MUID:20036896; PMID:10567266			
A:Accession: C75384			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-299 <WHI>			
A:Cross-references: UNIPROT:Q9RU61; GB:AE001997; GB:AE000513; NID:g6459292; PIDN:AAF1109			
C:Genetics:			
A:Gene: DR1533			
A:Map position: 1			
Query Match			
Best Local Similarity 10.8%; Score 311.5; DB 2; Length 299;			
Matches 65; Conservative 34; Mismatches 50; Indels 21; Gaps 3;			
QY	155	HYGPIPGVGTMMRFVRVQVSESGVHRPHVAGIHGRSNDGSYSLVLAGGYEDVDHGNFF	214
Db	4	HFGAVGVVPGMAFVNRRQELRDAGVHLPTQAGISGSASEGADSVLSGGYEDDRDEGDI	63
QY	215	TYTSGGGRDLSGNKRTAEQSCDKLTNTNRALALNCFAPINDQEGAEAKDWSRGKPVVV	274
Db	64	LYTGEGRD-----PLTGHQVXPQQLVRGNLALAIS-----HRDGLPLRVT	104
QY	275	RNVGKSKKYAPAGNRYDGIYKVVKYWPKEKSGFLWRYLLRRDDDE	324
Db	105	RGHR--HSSQFSPQSGYAGLYRVDDHWRVGRSGFLWRFLTRLENQ	152
RESULT 8			
D84765			
similar to mammalian MHC III region protein G9a [imported] - Arabidopsis thaliana			
C:Species: Arabidopsis thaliana (mouse-ear cress)			
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004			
C:Accession: D84765			
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;			
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.			
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.			
Nature 402, 761-768, 1999			
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.			
A:Reference number: A84420; MUID:20083487; PMID:10617197			
A:Accession: D84765			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-794 <STO>			
A:Cross-references: UNIPROT:O82175; GB:AE002093; NID:g3668088; PIDN:AAC61820.1; GSPDB:GN			
C:Genetics:			
A:Gene: At2g35160			
A:Map position: 2			
Query Match			
Best Local Similarity 9.3%; Score 270.5; DB 2; Length 794;			
Matches 71; Conservative 43; Mismatches 92; Indels 35; Gaps 7;			
QY	103	NDASEVVLAGERLRESKK---NAKVASATSSSQRDWKGMCACVGRTECTIVPSNHYGPI	159

Db 281 --HQHKQCNQRLVGNLGM-----ERSMHYGIEVRVIRGI-----KYE 317
QY 287 PAEGNR---YDGIYKVVWPKGKSGFLVWRYLLRRDDDEP--GPWTKEGKDRIKKLGL 341
Db 318 NSTSKVYVYDGLYKIVDWWFAVGKSGFGVFRFLVRIEQPMGSAVMRFAQTLRNRP- 376
QY 342 TWQYPEGYLE-ALANRERKEN 362
Db 377 SMVRPTGYVSFDLSNK---KEN 395

RESULT 12
F96756
hypothetical protein F3N23.30 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96756
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96756
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-669 <STO>
A:Cross-references: GB:AE005173; NID:g55903099; PIDN:AAD55657.1; GSPDB:GN00141
C:Genetics:
A:Gene: F3N23.30
A:Map position: 1

Query Match 6.7%; Score 194.5; DB 2; Length 669;
Best Local Similarity 29.5%; Pred. No. 8.6e-06;
Matches 67; Conservative 31; Mismatches 92; Indels 37; Gaps 8;

QY 157 GPIPGIPVGTWFRFRVQVSESGVHRPHVAGI-----GRSNDG-SYSLVLAGGYEDVD 209
Db 208 GTVPGLEVGDIFSRFEMCLVGLHMQTMAGIDYIISKAGSDSEIATISVSSGRGEQAQ 267
QY 210 HGNFYTTSGGRDLSGNKRTAEQSCDQKLTNTNRALALNCFAPINDQEGAEAKDWRSGK 269
Db 268 DPESLIYSGG-----GNADKNRQASDQKLERGNLAL-----ENSLRKN 307
QY 270 PVRVVRNVGKNSKYAPAEGRNYDGIYKVVWPKGKSGFLVWRYLLRRDDDEP---G 326
Db 308 GVRVVR---GEEDAASKTKIYIDGLYISGSWEKSGGCTFKYKLVRFQGPAPFG 364
QY 327 PWTKEGKDRIKKLGLTMQYPEGYLEALANRERKENSKREEEQSQS 373
Db 365 FWKSQK---WKEGLTTR-PGLLPDLTSGAESKPVSLVNDVDEQK 407

RESULT 13
G86312
hypothetical protein F2H15.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: G86312
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86312
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-954 <STO>
A:Cross-references: GB:AE005172; NID:g9665056; PIDN:AAF97258.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 6.6%; Score 192.5; DB 2; Length 954;
Best Local Similarity 30.6%; Pred. No. 1.8e-05;
Matches 55; Conservative 28; Mismatches 58; Indels 39; Gaps 6;

QY 157 GPIPGIPVGTWFRFRVQVSESGVHRPHVAGI-----HGRSNDGSYSLVLAGGYEDVD 209
Db 227 GAVPGIHYVDIFYYWGENCLVGLHKSNGYGGIDFFTAESAVERGHAAAMCVVTAGQYDGETE 286
QY 210 HGNFYTTSGGRDLSGNKRTAEQSCDQKLTNTNRALALNCFAPINDQEGAEAKDWRSGK 269
Db 287 GLDTLIYSGQGTDVYGNAR-----DOEMKGGNLAL-----EASVSK---GN 325
QY 270 PVRVVRNVGKNSKYAPAEGRN---YDGIYKVVWPKGKSGFLVWRYLLRRDDDEP 325
Db 326 DVRVRGV-----IHPHENNQKIYYDGMVLSKFWTVTGKSGKFRFKLVKPNQP 378

RESULT 14
T03455
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03455
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano,
Oncogene 15, 549-560, 1997
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4957 <PRA>
A:Cross-references: UNIPROT:O14686; EMBL:AF010404; NID:g2358286; PIDN:AAC51735.1; PID:g2
C:Genetics:
A:Gene: ALR
A:Map position: 12
C:Superfamily: acute lymphoblastic leukemia protein, ALR type
C:Keywords: alternative splicing

Query Match 5.9%; Score 170; DB 2; Length 4957;
Best Local Similarity 20.3%; Pred. No. 0.0042;
Matches 120; Conservative 72; Mismatches 221; Indels 178; Gaps 27;

QY 1 DDLNDCRIIF--VDEVFKIE-----RPGEGSPMVDNPMRRKSGPSCKHKCDVN 48
Db 777 DDTMQNTVLESNTDKFVLMQDMCVVCGSFGRAEGHLLACSCQCYHPYCVNSKITKV 836
QY 49 RL-----CRVC-ACHLOGGRDPDKQLMCDCECDMAFIHYICLDPPILSSVPS ----- 92
Db 837 MLLKGWRCVECTVCEVCGQASDPSRLLLCDDCIDSYHTYICLDPPILPTVPKGWKCKCVS 896
QY 93 -----EDENY-----CPECND-ASEVVLAGEIRLRSKNAKWS 126
Db 897 CMQGAASPGFHCWQNSYTHGCPASLVUTCPICHAPVVEEDLLIQCHRCRMMHAGCES 956
QY 127 ATSSSQRDWG--KGMACVGRKTECTIVPSNHYGPITGPVGT-----MWRFR-VQVSES 177
Db 957 LFTEDDVDAHDEGDFDCVS-CQPYVVKVPAVPAPPELVPMKVKEPEQYFRFEGVWLJET 1015
QY 178 G-----VHR-----PHVAGIHGRSNDGSYSLVLAGGYEDVDHGNFFTF- 215
Db 1016 GMLLRNLTMPLHKRRQRRLGLGPGAGLEGSEGPSDALG-----PDDKKGDLDTD 1068

QY 216 --YTGSGRDLGKNTAEQSCDQKLTNTNRALALNCFAPIN-----DOEGAEAKDWRSG 268
Db 1069 ELLKGGG-----VEHMECEIKLE-----GPVSPDVEPGKEETEESKKRK 1109
QY 269 KPVK-----VVRNVKGGKNSKYP-AEGRNRYDGIYKVKYWPKEGKGFVWRYLLRRD 321
Db 1110 KPYRPGIGFMVQRKSHTRTKGPAQAQAEVLGGQDPDEVIPADLPAGAVEQSL--AE 1167
QY 322 DDEPGPWTKEGDKRIKKGLTMTQYPEGYLEALANR----- 357
Db 1168 GDEKKKQRRGRKRSKLEGM---FPAYLQEAFFGKELLDLSRKALFAVGVGRPSFGLGTP 1224
QY 358 -----REKENSKR-----EEEEQEGGFASPTGKGKWKRSAGGSPSRAG 398
Db 1225 KAKGSGSERKELPTSQKGGDDPDIADEESRGLEGKADTPGEDGGVKASPVSPDPEKPG 1284
QY 399 SPRRTSKTKVPEYSLTAQSSLIREDKSNALWNEVLASLKDRP-ASGSP 448
Db 1285 TPGEGLSSDLDRIS-TEELPKM--ESKDLQQLFKDVLGSEREQHLGCGTP 1332

RESULT 15
T03454
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03454
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano,
Oncogene 15, 549-560, 1997
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03454
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-5262 <PRA>
A:Cross-references: UNIPROT:O14686; EMBL:AF010403; NID:g2358284; PIDN:AAC51734.1; PID:g2
C:Genetics:
A:Gene: ALR
A:Map position: 12
C:Superfamily: acute lymphoblastic leukemia protein, ALR type
C:Keywords: alternative splicing

Query Match 5.9%; Score 170; DB 2; Length 5262;
Best Local Similarity 20.3%; Pred. No. 0.0044;
Matches 120; Conservative 72; Mismatches 221; Indels 178; Gaps 27;

QY 1 DQSLNDCRIIF--VDEVFKIE-----RPGEGSPMVDNPMRKRKSPGSKCHKCKDDVN 48
Db 1082 DDTMONTVLFSTNDRKFLVLMQMCVVCGSFGRGAEGHLLACSCQCYHPYCVNSKITKV 1141
QY 49 RL-----CRVC-ACHLCGGGQDPDKOLMCDCECDMAFIYCLDPPLSVPS----- 92
Db 1142 MLLKMGWRCVCIVCVCGQASDPSRLLCDDCDSYHTYCLDPPLLTPVPGKWKCKVCVS 1201
QY 93 -----EDEWY-----CPECRND-ASEVVLAGERLERESKKNAKMAS 126
Db 1202 CMQCGAASPGFCEWQNSYTHCGPCASLVTCPICHAPYVEEDLLIOCRHCEWMAHAGCES 1261
QY 127 ATSSSQDNG--KGMACVGRKTECTIVPSNHYGPIPIGIVGT-----MWRFR-VQVSES 177
Db 1262 LFTEDDDVDHAPDEGDFCVS-CQPVVVKVAPVAPPVLPVPMKVKEPEPQVFRFEGVWLTTET 1320
QY 178 G-----VHR-----PHVAGIHRSDNGSYSLVLAGYEDVDHGNFFT- 215
Db 1321 GMAALLNLMTSLPHKRRQRRLGLFCEAGLEGSEPSDALG-----PDDKKGGLDSTD 1373
QY 216 --YTGSGRDLGKNTAEQSCDQKLTNTNRALALNCFAPIN-----DOEGAEAKDWRSG 268
Db 1374 ELLKGGG-----VEHMECEIKLE-----GPVSPDVEPGKEETEESKKRK 1414
QY 269 KPVK-----VVRNVKGGKNSKYP-AEGRNRYDGIYKVKYWPKEGKGFVWRYLLRRD 321
Db 1415 KPYRPGIGFMVQRKSHTRTKGPAQAQAEVLGGQDPDEVIPADLPAGAVEQSL--AE 1472

QY 322 DDEPGPWTKEGDKRIKKGLTMTQYPEGYLEALANR----- 357
Db 1473 GDEKKKQRRGRKRSKLEGM---FPAYLQEAFFGKELLDLSRKALFAVGVGRPSFGLGTP 1529
QY 358 -----REKENSKR-----EEEEQEGGFASPTGKGKWKRSAGGSPSRAG 398
Db 1530 KAKGSGSERKELPTSQKGGDDPDIADEESRGLEGKADTPGEDGGVKASPVSPDPEKPG 1589
QY 399 SPRRTSKTKVPEYSLTAQSSLIREDKSNALWNEVLASLKDRP-ASGSP 448
Db 1590 TPGEGLSSDLDRIS-TEELPKM--ESKDLQQLFKDVLGSEREQHLGCGTP 1637

Search completed: July 25, 2005, 17:07:33
Job time : 45 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 25, 2005, 17:00:57 ; Search time 158 Seconds
(without alignments)
1307.310 Million cell updates/sec

Title: US-10-019-071-2_COPY_263_793

Perfect score: 2896

Sequence: 1 DDSLNDLCRIIFVDFVKIER.....VNQPLQTLVNLQPLPGYGNR 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2896	100.0	793	16	US-10-751-736-115
2	2887	99.7	793	14	US-10-123-568-2
3	2887	99.7	793	15	US-10-188-832-27
4	2887	99.7	793	16	US-10-370-7158-456
5	2815	97.2	780	15	US-10-295-027-156
6	1718.5	59.3	802	16	US-10-476-924-7
7	1297	44.8	645	15	US-10-126-103-113
8	1297	44.8	645	15	US-10-431-096-113
9	823.5	28.4	198	9	US-09-867-550-766
10	736	25.4	136	14	US-10-123-568-3
11	672	23.2	133	9	US-09-764-864-1301

ALIGNMENTS

RESULT 1
US-10-751-736-115
; Sequence 115, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: CANCERS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-751-736-115

Query Match 100.0%; Score 2896; DB 16; Length 793;
Best Local Similarity 100.0%; Pred. NO. 1.7e-233;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DDSLNDLCRIIFVDFVKIERPGESPMVDNPMRRKSGPSCKKDDVNLRCVCACHLCG 60
DB 263 DDSLNDLCRIIFVDFVKIERPGESPMVDNPMRRKSGPSCKKDDVNLRCVCACHLCG 322
QY 61 GQDDPDQKLMCDCEMDAFHYICLDPLSSVPSDEWYCPCECRNDASEVVLAGELRRESKK 120

Sequence 39797, A
Sequence 174378, A
Sequence 174378, A
Sequence 522, App
Sequence 2314, App
Sequence 156872, A
Sequence 180766, A
Sequence 1309, App
Sequence 848, App
Sequence 263042, A
Sequence 132977, A
Sequence 333474, A
Sequence 41693, A
Sequence 6821, App
Sequence 322796, A
Sequence 54293, A
Sequence 277747, A
Sequence 15064, A
Sequence 15058, A
Sequence 167978, A
Sequence 109882, A
Sequence 57455, A
Sequence 600, App
Sequence 545, App
Sequence 171858, A
Sequence 145990, A
Sequence 15065, A
Sequence 133503, A
Sequence 70940, A
Sequence 267706, A
Sequence 33924, A
Sequence 296869, A
Sequence 159376, A
Sequence 72673, A

Db 323 GRQDPDKQLMCDCEMDAFHIYCLDPLSSVPSEDEWYCPCRNDASEVVLAGERLESKK 382
QY 121 NAKMASATSSORDWKGKMACVGRTECTIIVPSNHYGPIPGIPVGTMMRFRVQVSESGVH 180
Db 383 NAKMASATSSORDWKGKMACVGRTECTIIVPSNHYGPIPGIPVGTMMRFRVQVSESGVH 442
QY 181 RPHVAGIHGRSNDGYSYSLVLAGYEDDVHGNFFVTYTGSGRDLGSKNKTABQSCDQKLT 240
Db 443 RPHVAGIHGRSNDGYSYSLVLAGYEDDVHGNFFVTYTGSGRDLGSKNKTABQSCDQKLT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNRYDGIYKV 300
Db 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNRYDGIYKV 562
QY 301 KYWPEKGSGFLVWRYLLRRDDDEPGPWTKEGKDRIKKLGLTMQYPEGYLEALANREREK 360
Db 563 KYWPEKGSGFLVWRYLLRRDDDEPGPWTKEGKDRIKKLGLTMQYPEGYLEALANREREK 622
QY 361 ENSKREEREOQGGFASPRITGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 420
Db 623 ENSKREEREOQGGFASPRITGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 682
QY 421 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFOCICQOELVFRPITTVCOHN 480
Db 683 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFOCICQOELVFRPITTVCOHN 742
QY 481 VKDCCLDRSFRAQVFCSPACRYDLGRSYAMQVNPLOTVLNQLPFGYGNR 531
Db 743 VKDCCLDRSFRAQVFCSPACRYDLGRSYAMQVNPLOTVLNQLPFGYGNR 793
RESULT 2
US-10-123-568-2
; Sequence 2, Application US/10123568
; Publication No. US20030194713A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: NP95: Methods of Assaying for Cell Cycle Modulators
; FILE REFERENCE: 021044-003400US
; CURRENT APPLICATION NUMBER: US/10/123,568
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human NP95 nuclear zinc finger protein
US-10-123-568-2

Query Match 99.7%; Score 2887; DB 14; Length 793;
Best Local Similarity 99.6%; Pred. No. 9.8e-233;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDSLNDRCRIIFVDEVFKIERPGEPSPMVDNPMRRKSGPSCKHKCKDDVNRLCRVACHLCG 60
Db 263 DDSLNDRCRIIFVDEVFKIERPGEPSPMVDNPMRRKSGPSCKHKCKDDVNRLCRVACHLCG 322
QY 61 GRQDPDKQLMCDCEMDAFHIYCLDPLSSVPSEDEWYCPCRNDASEVVLAGERLESKK 120
Db 323 GRQDPDKQLMCDCEMDAFHIYCLDPLSSVPSEDEWYCPCRNDASEVVLAGERLESKK 382
QY 121 NAKMASATSSORDWKGKMACVGRTECTIIVPSNHYGPIPGIPVGTMMRFRVQVSESGVH 180
Db 383 NAKMASATSSORDWKGKMACVGRTECTIIVPSNHYGPIPGIPVGTMMRFRVQVSESGVH 442
QY 181 RPHVAGIHGRSNDGYSYSLVLAGYEDDVHGNFFVTYTGSGRDLGSKNKTABQSCDQKLT 240
Db 443 RPHVAGIHGRSNDGAYSLVLAGYEDDVHGNFFVTYTGSGRDLGSKNKTABQSCDQKLT 502

QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNRYDGIYKV 300
Db 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNRYDGIYKV 562
QY 301 KYWPEKGSGFLVWRYLLRRDDDEPGPWTKEGKDRIKKLGLTMQYPEGYLEALANREREK 360
Db 563 KYWPEKGSGFLVWRYLLRRDDDEPGPWTKEGKDRIKKLGLTMQYPEGYLEALANREREK 622
QY 361 ENSKREEREOQGGFASPRITGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 420
Db 623 ENSKREEREOQGGFASPRITGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 682
QY 421 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFOCICQOELVFRPITTVCOHN 480
Db 683 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFOCICQOELVFRPITTVCOHN 742
QY 481 VKDCCLDRSFRAQVFCSPACRYDLGRSYAMQVNPLOTVLNQLPFGYGNR 531
Db 743 VKDCCLDRSFRAQVFCSPACRYDLGRSYAMQVNPLOTVLNQLPFGYGNR 793
RESULT 3
US-10-188-832-27
; Sequence 27, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-27

Query Match 99.7%; Score 2887; DB 15; Length 793;
Best Local Similarity 99.6%; Pred. No. 9.8e-233;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDSLNDRCRIIFVDEVFKIERPGEPSPMVDNPMRRKSGPSCKHKCKDDVNRLCRVACHLCG 60
Db 263 DDSLNDRCRIIFVDEVFKIERPGEPSPMVDNPMRRKSGPSCKHKCKDDVNRLCRVACHLCG 322
QY 61 GRQDPDKQLMCDCEMDAFHIYCLDPLSSVPSEDEWYCPCRNDASEVVLAGERLESKK 120
Db 323 GRQDPDKQLMCDCEMDAFHIYCLDPLSSVPSEDEWYCPCRNDASEVVLAGERLESKK 382
QY 121 NAKMASATSSORDWKGKMACVGRTECTIIVPSNHYGPIPGIPVGTMMRFRVQVSESGVH 180
Db 383 NAKMASATSSORDWKGKMACVGRTECTIIVPSNHYGPIPGIPVGTMMRFRVQVSESGVH 442
QY 181 RPHVAGIHGRSNDGYSYSLVLAGYEDDVHGNFFVTYTGSGRDLGSKNKTABQSCDQKLT 240
Db 443 RPHVAGIHGRSNDGAYSLVLAGYEDDVHGNFFVTYTGSGRDLGSKNKTABQSCDQKLT 502

Qy	241	NTN	R	A	L	A	L	C	F	A	P	I	N	D	O	G	E	A	K	O	W	R	S	K	P	V	R	V	R	N	V	G	G	R	K	S	K	V	A	P	A	E	G	N	R	I	D	G	I	Y	K	V		300						
Db	503	NTN	R	A	L	A	L	C	F	A	P	I	N	D	O	G	E	A	K	O	W	R	S	K	P	V	R	V	R	N	V	G	G	R	K	S	K	V	A	P	A	E	G	N	R	I	D	G	I	Y	K	V		562						
Qy	301	K	Y	P	E	K	G	K	G	S	G	F	L	V	W	R	Y	L	L	R	D	D	E	P	G	P	T	K	E	G	K	D	R	I	K	K	L	G	L	T	M	Q	P	E	G	Y	L	E	A	L	A	N	R	E	K		360			
Db	563	K	Y	P	E	K	G	K	G	S	G	F	L	V	W	R	Y	L	L	R	D	D	E	P	G	P	T	K	E	G	K	D	R	I	K	K	L	G	L	T	M	Q	P	E	G	Y	L	E	A	L	A	N	R	E	K		622			
Qy	361	E	N	S	K	R	E	E	E	E	O	E	G	G	P	A	S	P	R	T	G	K	W	K	R	S	A	G	G	P	S	R	A	G	S	P	R	T	S	K	T	K	V	E	P	S	L	T	A	Q	S		420							
Db	623	E	N	S	K	R	E	E	E	O	E	G	G	P	A	S	P	R	T	G	K	W	K	R	S	A	G	G	P	S	R	A	G	S	P	R	T	S	K	T	K	V	E	P	S	L	T	A	Q	S		682								
Qy	421	L	I	R	E	D	K	S	N	A	K	L	W	N	E	V	I	A	S	L	K	O	R	P	A	S	G	S	P	F	O	L	F	L	S	K	V	E	E	T	F	O	C	I	C	O	E	L	V	F	R	I	T	T	V	C	Q	N		480
Db	683	L	I	R	E	D	K	S	N	A	K	L	W	N	E	V	I	A	S	L	K	O	R	P	A	S	G	S	P	F	O	L	F	L	S	K	V	E	E	T	F	O	C	I	C	O	E	L	V	F	R	I	T	T	V	C	Q	N		742
Qy	481	V	K	C	D	L	D	R	S	F	R	A	O	V	F	C	P	A	C	R	Y	D	L	G	R	S	V	A	M	O	V	N	O	P	L	O	T	V	N	L	N	L	F	P	G	Y	G	N	G	R		531								
Db	743	V	K	C	D	L	D	R	S	F	R	A	O	V	F	C	P	A	C	R	Y	D	L	G	R	S	V	A	M	O	V	N	O	P	L	O	T	V	N	L	N	L	F	P	G	Y	G	N	G	R		793								

```

RESULT 4
US-10-370-715B-456
; Sequence 456, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
;   Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 456
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-456

```

Query Match	99.7%;	Score 2887;	DB 16;	Length 793;
Best Local Similarity	99.6%;	Pred. No. 9.8e-233;		
Matches 529;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	DDSLNDCRILIFVDEVPKIERPGE	GGPMVDNPNRRKSGSPCKCKKDQD	VNRLCRVCACHLCG 60
Db	263	DDSLNDCRILIFVDEVPKIERPGE	GGPMVDNPNRRKSGSPCKCKKDQD	VNRLCRVCACHLCG 322
Qy	61	GRQPDKQIMCEDCDMAFHIYCLD	PLSPVSEDEWYCPCENDASEVVL	AGERLESKK 120
Db	323	GRQPDKQIMCEDCDMAFHIYCLD	PPLSPVSEDEWYCPCENDASEVVL	AGERLESKK 382
Qy	121	NAKMASATSSSSORDMGKGMAC	VGRTKECTIVPSNHYGP	IPGIPVGTMTWFRVQVSESGVH 180
Db	393	NAKMASATSSSSORDMGKGMAC	VGRTKECTIVPSNHYGP	IPGIPVGTMTWFRVQVSESGVH 442
Qy	181	RPHVAGIHGRSNDGYSYSLV	LAGGYEDVDVHGNYFTYTGSGGRD	LSGNKRTAQSCDQKLT 240
Db	443	RPHVAGIHGRSNDGAYSLV	LAGGYEDVDVHGNYFTYTGSGGRD	LSGNKRTAQSCDQKLT 502
Qy	241	NTNRALALNCFAPINDQEGAEAK	WRSGKPVVRVNRVKGKGNKYPAP	AEGRNDYDGIIYKV 300
Db	503	NTNRALALNCFAPINDQEGAEAK	WRSGKPVVRVNRVKGKGNKYPAP	AEGRNDYDGIIYKV 562
Qy	301	KYWPCKGSGFLVWRYLLRRDD	DEPCPMTKEGDKRIKGLT	WTQYPEGYLEALANRREK 360

```

Db      563 KYWEKSGKSGFLVWRYLLRRDDDPGWTKGKDRIKILGLTQMYPGYLELANRERBK 622
Qy      361 ENSKREBEEOEGGFASPRTKGKWKRSAGGSPSRAGSPRRTSKTKTVEPYSLTAQOSS 420
Db      623 ENSKREBEEOEGGFASPRTKGKWKRSAGGSPSRAGSPRRTSKTKTVEPYSLTAQOSS 682
Qy      421 LIREDKSNKLNWEVLASLDRPASGSPFQLFLSKVETFOCICQELVFRPITTVCOHN 480
Db      683 LIREDKSNKLNWEVLASLDRPASGSPFQLFLSKVETFOCICQELVFRPITTVCOHN 742
Qy      481 VKCDCLDRSFRAQVFSFACRYDILGRSYAMOVNQPLQTLVNLQFLPGYNGR 531
Db      743 VKCDCLDRSFRAQVFSFACRYDILGRSYAMOVNQPLQTLVNLQFLPGYNGR 793

RESULT 5
US-10-295-027-156
; Sequence 156, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 780
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-295-027-156

```

Query Match	97.2%	Score	2815	DB	15	Length	780
Best Local Similarity	99.6%	Pred.	No. 1e-226				
Matches	516	Conservative	1	Mismatches	1	Indels	0
Gaps	0						
Qy	1	DDSLNDCRIIIFVDVFVKIERGEGSPWVDNPMRRKSGPSCKHKDDVNRLCVCA	HLGG	60			
Db	263	DDSLNDCRIIIFVDVFVKIERGEGSPWVDNPMRRKSGPSCKHKDDVNRLCVCA	HLGG	322			
Qy	61	GRQDPDKQLMCDECDMAFIHYCLDPPASSVPSESDWYCPGCRNDASEVVL	LAGERLRESKK	120			

Db 323 GRQDPDKQLMCDCEMAFHYICLDPLSSVPSEDEWYCEPCRNDADEVVLGRLRESCK 382
Qy 121 NAKMASATSSORDWKGCMACVGRTEKCTIVPSNHYGPPIPGIPVGTWMPFRVQVSEGVH 180
Db 383 KAKMASATSSORDWKGCMACVGRTEKCTIVPSNHYGPPIPGIPVGTWMPFRVQVSEGVH 442
Qy 181 RHVAGIHGRSNDGYSVLVAGYEDDVHGNFFTYTSGGRDLGSKNKTAEOSCDOKLT 240
Db 443 RHVAGIHGRSNDGYSVLVAGYEDDVHGNFFTYTSGGRDLGSKNKTAEOSCDOKLT 502
Qy 241 NTNRLALALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNYDGIYKV 300
Db 503 NTNRLALALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNYDGIYKV 562
Qy 301 KYWPEKGKSGFLVWRYLLRRDDDEPGPWTKEGKDRIKKLGLTMQYPEGYLEALANREK 360
Db 563 KYWPEKGKSGFLVWRYLLRRDDDEPGPWTKEGKDRIKKLGLTMQYPEGYLEALANREK 622
Qy 361 ENSKREEEEOQGGFASPTGKGKWKRSAGGSPRAGSPRSTSKTKVPEYSLTAQOSS 420
Db 623 ENSKREEEEOQGGFASPTGKGKWKRSAGGSPRAGSPRSTSKTKVPEYSLTAQOSS 682
Qy 421 LIREDKSNKLNWNEVLASLKDPRASGPFQFLSKVEETFOCICCOELVFRPITTVCOHN 480
Db 683 LIREDKSNKLNWNEVLASLKDPRASGPFQFLSKVEETFOCICCOELVFRPITTVCOHN 742
Qy 481 VKKCLDRSFRAQVFCPCRYDLGRSYAMQVNPLOQT 518
Db 743 VKKCLDRSFRAQVFCPCRYDLGRSYAMQVNPLOQT 780

RESULT 6

US-10-476-924-7
; Sequence 7, Application US/10476924
; Publication No. US20040152093A1
; GENERAL INFORMATION:
; APPLICANT: YUE, Henry; DING, Li;
; APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
; APPLICANT: YUE, Huibin; HAFALIA, April J.A.;
; APPLICANT: LEE, Ernestine A.; ISON, Craig H.;
; APPLICANT: BECHA, Shanya D.; GURURAJAN, Rajagopal;
; APPLICANT: EMERLING, Brooke M.; GRIFFIN, Jennifer A.;
; APPLICANT: TANG, Y. Tom; LU, Dyung Aina M.;
; APPLICANT: YAO, Monique G.; CHAMLA, Narinder K.;
; APPLICANT: RAMKUMAR, Jayalaxmi; GANDHI, Ameena R.;
; APPLICANT: LEE, Soo Yeun; RICHARDSON, Thomas W.;
; APPLICANT: YANG, Junming; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; THANGAVELU, Kavitha;
; APPLICANT: HE, Ann; AZIMZAI, Valda;
; APPLICANT: RAUMANN, Brigitte E.; SWARNAKAR, Anita;
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: NUCLEIC ACID-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0960 USN
; CURRENT APPLICATION NUMBER: US/10/476,924
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/US02/14276
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 60/288,598
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/291,776
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/292,172
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/293,564
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 4706628CD1
US-10-476-924-7
Query Match 59.3%; Score 1718.5; DB 16; Length 802;
Best Local Similarity 59.2%; Pred. No. 8.4e-135;
Matches 316; Conservative 77; Mismatches 116; Indels 25; Gaps 6;
Qy 1 DDSLNDCHRIIFVDEVFVKIERPEGSPM--VNPMPRKSGPSCKHCKDDVNLRCVACHL 58
Db 291 EGTLNDCKIISVDEIFKIERPG-AHPLSFADGKFLRRNDPECDLCGGPCKKCHSCSRV 349
Qy 59 CGGRDDPKQLMCDCEMAFHYICLDPLSSVPSEDEWYCEPCRNDADEVVLGRLRES 118
Db 350 CGGRHEPNMQLDCECNVAYHYICLNPPLDKVPBEEYWCPSCKTDSSESVKAGRLKMS 409
Qy 119 KKNAMASATSSORDWKGCMACVGRTEKCTIVPSNHYGPPIPGIPVGTWMPFRVQVSEBG 178
Db 410 KKKAKMPASASTESRRDWMGRMACVGRTECTIVPSNHYGPPIPGIPVGTWMPFRVQVSEAG 469
Qy 179 VHRHVAGIHGRSNDGYSVLVAGYEDDVHGNFFTYTSGGRDLGSKNKTAEOSCDOK 238
Db 470 VHRHVAGIHGRSNDGYSVLVAGYEDDVHGNFFTYTSGGRDLGSKNKTAEOSCDOK 529
Qy 239 LTNTNRLALALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNYDGIYK 298
Db 530 LTNTNRLALALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNYDGIYK 589
Qy 299 VVKYWEPEKGS-GFLVWRYLLRRDDDEPGPWTKEGKDRIKKLGLTMQYPEGYLEALANRE 357
Db 590 VVKYWEPELSSSHGFLVWRYLLRRDDDEPGPWTSEGIERSRRLCLRLQYPAGY----PSD 644
Qy 358 REKENSKEEEEOQGGFASPTGKGKWKRSAGGSPRAGSPRSTSKTKVPEYSLTAQ 417
Db 645 KEGKKPKQSKKQPSGTTKRP-----ISDDDCPSASKYKASDAEAIEAFQLTPQ 695
Qy 418 QSSLIREDKSNKLNWNEVLASLKDPRASGPFQFLSKVEETFOCICCOELVFRPITTV 477
Db 696 QOHLIREDCQNKQLWDEVLSHLVEGPN-----FLKKLEQSFMCVCCQELVYQVPTTEC 748
Qy 478 QHNVCCKCLDRSFRAQVFCPCRYDLGRSYAMQVNPLOQTVNLQLPFGYGNGR 531
Db 749 FHNVCCKCLDRSFRAQVFCPCRYDLGRSYAMQVNPLOQTLLDLFFFGYSGKR 802
RESULT 7
US-10-126-103-113
; Sequence 113, Application US/10126103
; Publication No. US20030224486A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHWAY
; FILE REFERENCE: D0108.np
; CURRENT APPLICATION NUMBER: US/10/126,103
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/284,962
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 60/286,645
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/346,986
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: Patent version 3.0
; SEQ ID NO 113
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-126-103-113
Query Match 44.8%; Score 1297; DB 15; Length 645;
Best Local Similarity 67.2%; Pred. No. 1.3e-99;
Matches 231; Conservative 48; Mismatches 61; Indels 4; Gaps 3;


```
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:GI-2635
US-10-123-568-3

Query Match      25.4%; Score 736; DB 14; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.7e-53;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 AQSQCDKLTNTNRALALNCFAPINDQGAELKADWRSKPVVRVNRVKGKSKYAPAEQ 290
Db 1 AQSQCDKLTNTNRALALNCFAPINDQGAELKADWRSKPVVRVNRVKGKSKYAPAEQ 60

QY 291 NRYDGIYKVVKWPKEKSGFLVWRYLLRRDDDEPGWTKGDKRIKKGLTMQYPEGYL 350
Db 61 NRYDGIYKVVKWPKEKSGFLVWRYLLRRDDDEPGWTKGDKRIKKGLTMQYPEGYL 120

QY 351 EALANRERKENSKE 366
Db 121 EALANRERKENSKE 136

RESULT 11
US-09-764-864-1301
; Sequence 1301, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ23
; CURRENT APPLICATION NUMBER: US/09/764,864
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1301
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1301

Query Match      23.2%; Score 672; DB 9; Length 133;
Best Local Similarity 99.2%; Pred. No. 3.8e-48;
Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 405 KTKVEPYSILTAQSSLIREDKSNKALWNEVLASLKDRPASGSPFOLFSLKVEETPQCIC 464
Db 7 KTKVEPYSILTAQSSLIREDKSNKALWNEVLASLKDRPASGSPFOLFSLKVEETPQCIC 66

QY 465 COELVERPITTVCOHNVKCDLDRSPRAQVFSQACRYDLGRSYAMQVNOPLQTVLNOLF 524
Db 67 COELVERPITTVCOHNVKCDLDRSPRAQVFSQACRYDLGRSYAMQVNOPLQTVLNOLF 126

QY 525 PGYNGNR 531
Db 127 PGYNGNR 133

RESULT 12
US-10-425-114-39797
; Sequence 39797, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
```

```
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39797
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700763470_FLI.pep
US-10-425-114-39797

Query Match      21.6%; Score 626.5; DB 15; Length 694;
Best Local Similarity 28.1%; Pred. No. 2.3e-43;
Matches 180; Conservative 66; Mismatches 161; Indels 233; Gaps 21;

QY 55 ACHLCGRQDPDKQLMCDCEDMAPHIYCLDPLPSVPSDEWYCEC----- 101
Db 3 ACWVCKGLPGQERLLCVTCDTPWHVPCLFAPPPTLSATARWLCPCDSCILSDVPPVPAP 62

QY 102 -----RNDAS-----BVVLGAG----- 112
Db 63 ARNQLVAAMLAVENDASLTQHDKARKROELITGKAPADDDDDDEQENKSSLDILSRSLN 122

QY 113 -----ER-----LRESKKN-----AKMAS----- 126
Db 123 CSICIQLPERPVTSPCGHSFCLKCFEKWVRQGRKNCACROIIIPAKMTSQPRINSALVFA 182

QY 127 -----ATSSS-----ORDWKGKMACVGRTEKCTIVPSN 154
Db 183 IRMARQASNSGSGRGVRSVNHFLHNDQRPDEPTTERRAQSRGRANAASGKIFVTVPTD 242

QY 155 HYGPI-----PGIPVGTMRFRVQVSSGVHRPHVAGTHGRSNDGYSYLVLAGGYE 205
Db 243 HFGPITAENDPLRNOGLLVGESWRDLRCRWGAHFVPGVGGIAGQSDRGAQSVLSGGTV 302

QY 206 DDVDHGNFFTYTSGGRDLNKGRT-AEQSCDQKLTNTNRALALNCFAPINDQGAELKAD 264
Db 303 DDEHGEWFLYTGSGKDLNKGRTNKSFSFQKFKYNRALQVSL----- 349

QY 265 WRSGKPVVRVNRVKGKSKYAPAEGRNYDGIYKVVKWPKEKSGFLVWRYLLRRDDDE 324
Db 350 --QGYVVRVRSRK-EKRSYAPETGVRYDGIYRIEKCWQIAGLQGFVKVCYLFVRCNDE 406

QY 325 PGWTKGK-DRIKKGLTMQYPEGYLEALANRERKENSKEEBEQEGGFASPRITGK 383
Db 407 PAPWTSDDHGDPRPLPVI-----RELKKATVTHERTESPSWDF-DEEDSRW 452

QY 384 KWKRSKAGGSPRAGSPRRTSKTKVPEYSILTAQSSLIREDKSNKALWNEVLASLKDRP 443
Db 453 KWKRPSP--FSR-----QKVQNVPEVE-----VARAKSNKEVKFKLKSKE-- 492

QY 444 ASGSPFOLFSLKVEETFOCICQELVFRPITTVCOHNVKCDLDRSPRAQV----- 495
Db 493 -----QLQGFSCMICKEVWVSPVTTTCAHNFCKSCLEGEFAGQAFVKERSKGG 541

QY 496 -----SCPACRYDLGRSYA--MOVNOPLQTVLNOL 523
Db 542 RTLRSQKNVMKCPSCSIDIS-DYLQNIQVIDLKSAIESL 580

RESULT 13
US-10-424-599-174378
; Sequence 174378, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
```

APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 174378
LENGTH: 709
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_128482C.1.pap
US-10-424-599-174378

Query Match 21.6%; Score 626.5; DB 15; Length 709;
Best Local Similarity 28.1%; Pred. No. 2.3e-43;
Matches 180; Conservative 66; Mismatches 161; Indels 233; Gaps 21;
QY 55 ACHLCGRQDPKQMLMCDCEMAFIHYICLDPPLSSVPSDEWYCPCC-----101
DB 18 ACVCKGLPQBERLLCVTCDPWHVPCLFAPPTLSATARWLCPCDCLSDVDPVPAP 77
QY 102 -----RNDAS-----EVVLG-----112
DB 78 ARNQLVAANLAVENDASLTQHDKARKRQELLTKAPADDDDDDEQENKSSLSDSLRSUN 137
QY 113 -----ER-----LRESKN-----AKVAS-----126
DB 138 CSICILPBPVTPSCGHSFCLKCFEKVVRQGRNCAKCRQIIPAKWTQPRINSALVPA 197
QY 127 -----ATSSS-----QRDWKGKMACVGRTEKCTIVPSN 154
DB 198 IRMARQASNSGSGRGVRSVNHFLNQDRPDEPFTTERAQSRGRANAASGKIFVTVPD 257
QY 155 HVGPI-----POIPVGTWVRFRVQVSESGVHRPHVAGIHRNDSGYSILVAGGYE 205
DB 258 HFGPITAENDPLRNQGLLVGESWRDLRCQWGAHFVPVGGIAGQSDRGAQSVLGGYV 317
QY 206 DVDVHGNFTYTGSGGRDLSGNKRT-ABOSCOKLTNTNRALNCFAPINDOEGAEKD 264
DB 318 DDEHGEWFLYTGSGGRDLSGNKRTSHSPDQKFKYKRNALQVSL-----364
QY 265 WRSGKVRVVRNVKGGKSKYAPAEGRNYDGIYKVKYWPKEKSGFLVWYLLRDDDE 324
DB 365 --QGYFVRVVRSHK-EKRSYAPETGVYDGIYRIEKWCQIAGLQCFKVCYVLFVRCNE 421
QY 325 PGWTKEGK-DRIKKLGLTWQYPEGYLEALANRERKENSKEEEOQEGGFPASPTGK 383
DB 422 PAPWTSDDHGRPRPLFVI-----RELKATVIHERTESPSWDF-DEBDSRW 467
QY 384 KWKRSAGGSPSAGSPRSTKTKVBPYSLTAQSSLIREDKSNAKLWNEVLASLKDRP 443
DB 468 KWKKPPP--PSR-----QKQNVPEVE-----VARAKSNKVKKFLQSLIKE--507
QY 444 ASGSPFLSKVETFCQICCOELVPRPITTVCOHNVCKDCLDRSFRAQVF-----495
DB 508 -----QIQGFSCMICKEVMVSPVTTFCAHNFCKSLCEGEFAGQAFVKERSKG 556
QY 496 -----SCPACRYDLGRSYA--MQVNQPLQTVLNQL 523
DB 557 RTLRSQKVMKPCSCSIDIS-DYLNQIQVDIDLKSAIESL 595

RESULT 14
US-10-739-930-6375
Sequence 6375, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FILE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 6375
LENGTH: 645
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: Clone ID: ARATH-23APR03-C352_1.p
US-10-739-930-6375

Query Match 21.0%; Score 608; DB 16; Length 645;
Best Local Similarity 26.7%; Pred. No. 7.3e-42;
Matches 173; Conservative 69; Mismatches 161; Indels 246; Gaps 19;
QY 56 CHLCGRQDPKQMLMCDCEMAFIHYICLDPPLSSVPSDEWYCPCCRDNDASVVLG--112
DB 15 CMRCKSNPPRESLTGCTVTPWHVSCLSPPKTLASTLQWHCPDCSGEIDPLPVSAGAT 74
QY 113 -----ERLRESK-----119
DB 75 GFESAGSDLVAAIRAIAEADSLSTEKAKMRQLLSGKGVEDDEBEKKKKKGKGNPL 134
QY 120 -----119
DB 135 DVLSALGDNLMCSFCMQLPBPVTPKPCGHNACLKCFEKWGGQKRTCGKCRSIIPEKMAK 194
QY 120 -----KNAKMASATSS-----SORD-----WKGMAACVGR 145
DB 195 NPNRINSILVAIRLAKVSKSAATTSKVPHFISNDRDPDKAFTTERRAKTGTANAASG--252
QY 146 KECTIVPSNHYGPIP-----GIPVGTWVRFRVQVSESGVHRPHVAGIHRNDSGY 196
DB 253 KIYVTIPDPHFGPIPAENDPVRNQGILLVGESWEDRLECRQWGAHFPHVAGIAGQSTYGAQ 312
QY 197 SILVAGGYEDDVHGNFTYTGSGGRDLSGNKRT-ABOSCOKLTNTNRALNCFAPIN 255
DB 313 SVALSAGGYKDDHGEWFLYTGSGGRDLSGNKRTNKEQSFDQKFKSNAALKLSC-----367
QY 256 DQEGAEAKDWSGKVRVVRNVKGGKSKYAPAEGRNYDGIYKVKYWPKEKSG-FLVW 314
DB 368 -----KLGYPVRVVRSHK-EKRSYAPETGVYDGIYRIEKWCYVLFVRCNE 416
QY 315 RYLLRRDDDEPGWTK-EGKDRIKKGLTWQYPEGYLEALANRERKENSKEEEOQEG 373
DB 417 RYLFVRCNEPAPWTSDENGDRPRI--PNLPE--LNMAITDLPKERTPSWDFE----467
QY 374 GPASPTGKWKRSAGGSPSAGSPRSTKTKVBPYSLTAQSSLIREDKSNAKLWN 433
DB 468 -----GEGCWKM-----KPPPSKKS-----VNVLPABERKNLR---497
QY 434 EVLASLKDRPASGSPFLSKVETFCQICCOELVPRPITTVCOHNVCKDCLDRSF---490
DB 498 -----KATKAHNSNTMRALKLFKFCQICQVLTLPVTTPCAHNFCKACLEAKFAGK 549
QY 491 -----RAQVFCPACRYDLGRSYA--MQVNQPLQTVLNQL 523
DB 550 TLVRSRSTGRTLRSRKNVLCPCCTTDISDFLQNPQVNRVAVAEVIEKL 598

RESULT 15
US-10-225-066A-522
Sequence 522, Application US/10225066A
Publication No. US20030226173A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: DUBELL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: PILGRIM, Marsha L
APPLICANT: JIANG, Cai-Zhong

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 25, 2005, 16:56:22 ; Search time 43 Seconds
(without alignments)
921.829 Million cell updates/sec

Title: US-10-019-071-2_COPY_263_793
Perfect score: 2896
Sequence: 1 DBSLNDCRIIFVDFVKIER.....VNQLQTLNQLFPGYGNGR 531

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186.5	6.4	1400	US-09-764-176-7	Sequence 7, Appli
2	177	6.1	4019	US-09-854-133-425	Sequence 425, App
3	157.5	5.4	2079	US-09-949-016-8301	Sequence 8301, Ap
4	152.5	5.3	1935	US-09-949-016-10970	Sequence 10970, A
5	152	5.2	1674	US-09-418-710-1	Sequence 1, Appli
6	152	5.2	1674	US-09-839-479-1	Sequence 1, Appli
7	149	5.1	1673	US-09-418-710-70	Sequence 70, Appl
8	149	5.1	1673	US-09-839-479-69	Sequence 69, Appl
9	147	5.1	1527	US-09-418-710-27	Sequence 27, Appl
10	147	5.1	1527	US-09-839-479-27	Sequence 27, Appl
11	147	5.1	1531	US-09-418-710-29	Sequence 29, Appl
12	147	5.1	1531	US-09-839-479-29	Sequence 29, Appl
13	147	5.1	1540	US-09-949-016-7037	Sequence 7037, Ap
14	147	5.1	1722	US-09-538-092-1033	Sequence 1033, Ap
15	146.5	5.1	2289	US-09-051-019-2	Sequence 2, Appli
16	145.5	5.0	800	US-09-270-767-45282	Sequence 45282, A
17	143	4.9	1525	US-09-418-710-69	Sequence 69, Appl
18	143	4.9	1525	US-09-839-479-68	Sequence 68, Appl
19	143	4.9	1912	US-08-913-832A-2	Sequence 2, Appli
20	143	4.9	1912	US-09-249-181A-2	Sequence 2, Appli
21	143	4.9	1912	US-09-158-707-2	Sequence 2, Appli
22	139	4.8	1969	US-09-418-710-72	Sequence 72, Appl
23	139	4.8	1969	US-09-839-479-71	Sequence 71, Appl
24	139	4.8	1972	US-09-418-710-21	Sequence 21, Appl
25	139	4.8	1972	US-09-839-479-21	Sequence 21, Appl
26	138.5	4.8	45	US-09-839-479-44	Sequence 44, Appl
27	138.5	4.8	351	US-07-945-295-2	Sequence 2, Appli

28	138.5	4.8	351	5	PCT-US91-06418-1	Sequence 1, Appli
29	138.5	4.8	504	4	US-09-270-767-45920	Sequence 45920, A
30	138	4.8	386	4	US-09-764-176-3	Sequence 3, Appli
31	137.5	4.7	371	3	US-09-233-342A-5	Sequence 5, Appli
32	135.5	4.7	391	4	US-09-538-092-1369	Sequence 1369, Ap
33	135.5	4.7	391	4	US-09-949-016-6711	Sequence 6711, Ap
34	135.5	4.7	391	4	US-09-949-016-7788	Sequence 7788, Ap
35	135.5	4.7	405	2	US-08-881-857-2	Sequence 2, Appli
36	135.5	4.7	405	3	US-09-233-342A-2	Sequence 2, Appli
37	134.5	4.6	45	4	US-09-418-710-43	Sequence 43, Appl
38	134.5	4.6	45	4	US-09-418-710-56	Sequence 56, Appl
39	134.5	4.6	45	4	US-09-839-479-42	Sequence 42, Appl
40	134.5	4.6	45	4	US-09-839-479-55	Sequence 55, Appl
41	131.5	4.5	45	4	US-09-418-710-45	Sequence 45, Appl
42	131	4.5	44	4	US-09-418-710-58	Sequence 58, Appl
43	131	4.5	44	4	US-09-839-479-57	Sequence 57, Appl
44	127	4.4	594	4	US-09-949-016-9261	Sequence 9261, Ap
45	125.5	4.3	835	4	US-09-949-016-9685	Sequence 9685, Ap

ALIGNMENTS

RESULT 1

US-09-764-176-7
; Sequence 7, Application US/09764176
; Patent No. 6809189
; GENERAL INFORMATION:
; APPLICANT: NOTEBORN, Mathieu Hubertus Maria
; APPLICANT: DANEN-VAN OORSCHOT, Astrid Adriana Anna Maria
; APPLICANT: ROHN, Jennifer Leigh
; APPLICANT: WEISS, Bertram
; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
; FILE REFERENCE: 4735US
; CURRENT APPLICATION NUMBER: US/09/764,176
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Sequence: Amino acid sequence deduced from the nu
; OTHER INFORMATION: leuc acid sequence of AAP-
US-09-764-176-7

Query Match	6.4%	Score 186.5;	DB 4;	Length 1400;
Best Local Similarity	19.5%	Pred. No. 3.5e-08;		
Matches	95;	Conservative 64;	Mismatches 168;	Indels 159;
Gaps	19;			
QY	56	CHLCGGRRDPPQKLMCDMCAFIHYCLDPPPLSSVPSDEWYCPCRNDRND-----	104	
Db	853	CKKCGLPNHPILLICDCSDGYHTACLRPPLMIIP-DGEWFCPCQHKLLCEKEEQQLQ 911		
QY	105	-----ASEVVLAG-----ERLESKNKAMASATSSQORD 134		
Db	912	DLIDVALKKERAERKERLVVVGISIEIIPQEPDFSEDQEKKKDKSKKANLLERS 971		
QY	135	WKGGMACVGRTECTIVPSNHVGPPIGPIVGTWTFRV-----QVSESGVIRPHVAGIH 188		
Db	972	-----TRTKKC-----ISYRFDEFDEAIDEAIEDIKEADGGGV- 1005		
QY	189	GRSDGYSYSLVAGGEDVDHGNFTVTYSGGRDLS-----GNKRTASQSCDQKLT 240		
Db	1006	GRGKDIS-----TTTGHGKDIISTILDEERKENKR-PORAAARAK 1045		
QY	241	NTNRALALNCFAPINDQEGAEAKWRSGKPVVRVNRVKGKNSKYAPAEGRNYDGIY---- 297		
Db	1046	KRRRLNDLSDSNLDEESEDSEDFKISDGSQDFVVSNDENPFDESEEDPPSNDSDTDFCSR 1105		
QY	298	-----KVQYTWPEKSGSGLVWYLLRRDDDEPGPWTKEGKORIKKLGTLTM 343		

Db 1106 RLRRHPSRPMQRRLRRTPKKYS-----DDEEE--ESEENSRSSESDFSD 1152
QY 344 QYPEGYLEANRERKENSKE-----EEEOEGGFASPTGKGKWRKKSAGGSPSRAGS 399
Db 1153 DFSDDFVE--TRRRSRNRQKQINYNKEDSESQSLRRGK-----BIRRVH 1199
QY 400 PRTSKTKTVEPY-SLTAQOSSLIREDKSNAL-----WNEVLASLKDRPASGSPQL 451
Db 1200 KRLSSSEESYLSKNSEDDELAKESKRSVRRGRSTDEYSE--ADEEEEBEGKPSRK 1257
QY 452 FLKSVE 457
Db 1258 RLHRIE 1263

RESULT 2

US-09-854-133-425
; Sequence 425, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 425
; LENGTH: 4019
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-133-425

Query Match 6.1%; Score 177; DB 4; Length 4019;
Best Local Similarity 21.6%; Pred. No. 1.4e-06;
Matches 109; Conservative 58; Mismatches 150; Indels 188; Gaps 25;
QY 51 CRVC-ACHLCGGRRQDPKOLMCDCEDMAPHIYCLDPLSSVSEDEM---YCEPCEN-DA 105
Db 59 CLECTVCEACGKATDPGRLLLLDCDDISYHTYCLDPLQTPV-KGGWKCKWCWCRHCGA 117
QY 106 SEVVLAGERLRESKKNAKMASATS-----SSQRDMGKMACVGRTECTIVPSNHYGPI 160
Db 118 TSAGLCEQNNYTCAPCASLSLSCPVCYRNRYREDLLIQC-----RQC----- 161
QY 161 GIPVGTWTRFRV-----QVSESG-----VHRPHVAGIHGRSNDGYSLSVLAG--G 203
Db 162 -----DRWHAVQNLNTEBEENVADIGFDCSMCRPYMPASNPVSDCCSSSLVAQIVT 216
QY 204 YEDVDVHGFFTYG-----SGRDLSG-----NKRFAEQSCDKLTNTNRLALNCFA 252
Db 217 KYKELDPKPYTYTQDGVCLTESGMTQLQSLTVTVPRKRKSKPKLKLIIQNQNSVAVLQTP 276
QY 253 PYNDQEG--AEAKDWRSGKPVVRVNVGKSKSYAPAEGRNYDGIYKVVKYWGKGGK 310
Db 277 DTQSEHSRQEMDDSRGE-----LMDCDGKSESS-----PEREAV- 312
QY 311 FLVMRYLLRDDDEPGWTKBEGKDRIKKUGLTMQYPEGYLEALANRERKENSKEEBEQ 370
Db 313 -----DDETKG---VEGTDGVKK-----RKRKPYRP 335
QY 371 QEGGF---ASPRFGCKWKWRKSAGGSPSRGSPRRTSKTKVPEYSLTAQOSSLIREDKS 427
Db 336 GIGGFMVRRSRGTQGGKTKR-----FQLFLSKVEETFOCICQELV 363
QY 428 NA-----KLWNEVLA-SLKDRPASGSP-----FQLFLSKVEETFOCICQELV 469

Db 364 GSISEQLPCRDDGWSQELPDTLVDSESVSTESTEKIKKRYRKRKNKLEETPPAY-LQEAF 422
QY 470 FRPITTVCOHNVCKDCLDRSFRQV 494
Db 423 FG-----KDLDTSRQSKI 436
RESULT 3
US-09-949-016-8301
; Sequence 8301, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8301
; LENGTH: 2079
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8301

Query Match 5.4%; Score 157.5; DB 4; Length 2079;
Best Local Similarity 32.0%; Pred. No. 3.6e-05;
Matches 48; Conservative 14; Mismatches 49; Indels 39; Gaps 9;
QY 38 PSC-KHKCD---DVNRL-----CRVC-ACHLCGGRRQDPKOLMCDCEDMAPHIYCLDPP 86
Db 252 PSCLAFCELTNTNVKALRWQIECTCSACRVQG--RNADNMLFCDSCURGFHMECCDDP 309
QY 87 LSSVFESEWCPECRNDASEVVLAGERLRESKK-----NAKMASATSSOR 133
Db 310 LSRMP-KGMWICQVCRPKKGRKLLHEKAAQIKRRYAPIGRPKNLQRLLSVTS---- 364
QY 134 DWGKMACVGR-----TKECTIVPSNH 155
Db 365 DEGSNNAFTGRGSPGRGQTKVCTTPSSGH 394

RESULT 4

US-09-949-016-10970
; Sequence 10970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10970
; LENGTH: 1935
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10970

Query Match 5.3%; Score 152.5; DB 4; Length 1935;
Best Local Similarity 20.5%; Pred. No. 9.6e-05;
Matches 91; Conservative 47; Mismatches 120; Indels 185; Gaps 22;

QY 39 SCKHC-----KDVNRLCRVACACHLCGRQDPDKQLM 70
DB 428 SCPHCKEGVQWEAKEEBEYEEBEGEKEBEDDHMBYCRVC-----KGGELLC 479

QY 71 CDCDMAFHIYCLDPLSPSEDEWYCPCERNDADEVVLG--ERLRSEKKNAKMASAT 128
DB 480 CDACISSYHHCINPLPDIPN-GEWLCPRC-----TCPVLKGRVQKILHWR-----525

QY 129 SSSQRDWGKMACVGRKTECTIVPSNHYGPIPGIPVGTWMTFRVQVSESGVHRPHVAGH 188
DB 526 -----WGEPVAV-----PAP-----QQADGNPDVPPRPQLQ 552

QY 189 GRSND-----GSYSLVLAGGYE--DDVDHGNFTTSGGRDL 224
DB 553 GRSREFFVWVGLSYWHCSWAKELQLEIFHLVMYRNYQRKNDMDPEPPLDY-GSGEDDG 611

QY 225 SGNKRTAEGSCQKLTNTNRALALNCFAINDQEGAEKD--WRSQ-KPVRVRNVKGGK 281
DB 612 KSDKR-----KVDPHYAEEMEEKYRFGIKP-----637

QY 282 NSKYAPAEGNRYDGIYKVVKY-WPEKSGSGLV-WRYLLRRDDDEPGPWTKEGDKRIKKL 339
DB 638 -----EMWTVHRIINHSVDKKGNYHLVKWRDL-----PYDQSTWEED-----675

QY 340 GLUTMQVPEGYLEALANREKENSKEEBEQEGGFPASPTGKGKWRKSAGGSPRAGS 399
DB 676 --EMNIP-----YEBHKQSYMRHRELIMGEDPAQPRKYKKKKKELQGDGPPS---S 722

QY 400 PRR-TSKKTKVPSYSLTAQSSSL 421
DB 723 PTNDPTVKYETQPRFITATGGTL 745

RESULT 5
US-09-418-710-1
; Sequence 1, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-1

Query Match 5.2%; Score 152; DB 4; Length 1674;
Best Local Similarity 17.9%; Pred. No. 8.6e-05;
Matches 87; Conservative 61; Mismatches 144; Indels 194; Gaps 20;

QY 56 CHLCGRQDPDKQLMCDCEDMAFHIYCLDPLSPSEDEWYCPCERNDADEVVLGRL 115
DB 1269 CKICRKGDAENNVLCDCGRGHHTYCVRPKLTVP-EGDWFCEPCR-----1314

QY 116 RESKKNAKMASATSSSQDWGKMACVGRKTECTIVPSNHYGPIPGIPVGTWMTFRVQVS 175
DB 1315 --PKQRCRLS-----FR-----1325

QY 176 ESGVHRPHVAGIHGRSNDGYSVSLVLAGGYEDVDVHGNFTTYTSGGRDLGSKNRTAEQSC 235
DB 1326 ---QRPSES-----DEDVEDSM---GGEDDEV-----GDEBEGQSBEVEEV 1363

QY 236 DOKLTNTNRALALNCFAINDQEGAEKDWRSQKP-VRVVRNVKGGKSKYAPAEGNRYD 294
DB 1364 EODEDS-----QEBEVS LPKRGPQVRLPVKTRKJLSSFSRSSRQQQBP 1409

QY 295 GIYKVVKYWPBK-----GKSGFLVMRYLLRRDDDEPGPWTKEGDKRIKKLG 340
DB 1410 GRV-----PSRSQOSTPKTVSSKTGRS-----LRKINSAPPTETKS-----LRIAS 1451

QY 341 LTMQVPEG-----VLEALANREKENSKEEBEQEGGFPASPTGKGKWRKSAGGSP 394
DB 1452 RSTRSHGFLQADVFLVVELLSPRRKRRGRKSANNTPENFPNFRVIATKSEQSRSVNI 1511

QY 395 S-----RAGSPRRSTKTKVPEYSLTAQSS-----LIREDKNA 429
DB 1512 ASKLSLQSESKRRCRQSPSPVTLGRRSSRQGGVHLSAFEQLVVELVRHDDS-- 1569

QY 430 KLVNEVLASLKDORPASGSPFOLFSLKVEETFCICQBLVFRPI-----TTVCQHN 481
DB 1570 --W-----PFLKLVSKI---QVPYDIKKPIALNIIREKVNKCEYKL 1608

QY 482 CKDCILD 487
DB 1609 ASEPID 1614

RESULT 6
US-09-839-479-1
; Sequence 1, Application US/09839479
; Patent No. 6727222
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-1

Query Match 5.2%; Score 152; DB 4; Length 1674;
Best Local Similarity 17.9%; Pred. No. 8.6e-05;
Matches 87; Conservative 61; Mismatches 144; Indels 194; Gaps 20;

QY 56 CHLCGRQDPDKQLMCDCEDMAFHIYCLDPLSPSEDEWYCPCERNDADEVVLGRL 115
DB 1269 CKICRKGDAENNVLCDCGRGHHTYCVRPKLTVP-EGDWFCEPCR-----1314

QY 116 RESKKNAKMASATSSSQDWGKMACVGRKTECTIVPSNHYGPIPGIPVGTWMTFRVQVS 175
DB 1315 --PKQRCRLS-----FR-----1325

QY 176 ESGVHRPHVAGIHGRSNDGYSVSLVLAGGYEDVDVHGNFTTYTSGGRDLGSKNRTAEQSC 235
DB 1326 ---QRPSES-----DEDVEDSM---GGEDDEV-----GDEBEGQSBEVEEV 1363

QY 236 DOKLTNTNRALALNCFAINDQEGAEKDWRSQKP-VRVVRNVKGGKSKYAPAEGNRYD 294

Db 1364 EQDEDS-----QEEEVSLPKGRQVRLPVKTRGKLSFSRQOQEP 1409
QY 295 GIYKVKVWPEK-----GKSGFLVMRYLLRRDDDEPGPWTKEGDKRIKLG 340
Db 1410 GR-----PSRSQOSTPKTTVSSKTGRS-----LRKINSAPPTETKS-----LRIAS 1451
QY 341 LTMQYPEG-----YLEALANRERENSKREBEEOQEGGFASPRTGKWKWKRSAGGCP 394
Db 1452 RSTRHSHGLQADVFLVVELLSPRKRGRKSANNTPNSPNFNFRIATKSSEQRSVNI 1511
QY 395 S-----RAGSPRRTSKTKVPEYSLTAQOSS-----LIREDKSNA 429
Db 1512 ASKLSLOESKRRCKRQSPSPVTLGRSSRGQGVHLSAFEQLVVELVRHDDS-- 1569
QY 430 KLNVEVLASLKDPAAGSGPFQFLSKVETFCICQQLVFRPI-----TTVCQHN 481
Db 1570 --W-----PFLKLVSKI-----QVPDYDIKKPIALNIIREKVNKCEYKL 1608
QY 482 CKDCLD 487
Db 1609 ASEFID 1614

RESULT 7

US-09-418-710-70
; Sequence 70, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 1673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-70

Query Match 5.1%; Score 149; DB 4; Length 1673;
Best Local Similarity 17.9%; Pred. No. 0.00017;
Matches 87; Conservative 60; Mismatches 145; Indels 194; Gaps 20;
QY 56 CHLCGRQDPDKQLMCDCEMFAHIYCLDPPILSSVPSDEWYCPCECRNDASEVVLAGERL 115
Db 1268 CKICRKKGAENMVLCDCDRGHHTYCVRPKLKIVP-EGDWFCPECR----- 1313
QY 116 RESKNAKMASATSSSQORDWKGMACVGRTECTIVPSNHYGPIGIPVGTWRRFRVQVS 175
Db 1314 --PKQRCRLS-----FR----- 1324
QY 176 ESGVHPHVAGIHGRSNDGSYSLVLAGVEDVDVHGNNFTYTGSGRDLSGNKRRTAEQSC 235
Db 1325 ----QRPSSLES-----DEDVEDSM-----GGBDDEVD-----GDEEGOSEEEYEV 1362
QY 236 DQKLTNTNRLALNCFAPINDQEGAEAKDWRSGKP-VRVVRNVKGGKNSKYAPAEGRYD 294
Db 1363 EQDEDS-----QEEEVSLPKGRQVRLPVKTRGKLSFSRQOQEP 1408
QY 295 GIYKVKVWPEK-----GKSGFLVMRYLLRRDDDEPGPWTKEGDKRIKLG 340
Db 1409 GR-----PSRSQOSTPKTTVSSKTGRS-----LRKINSAPPTETKS-----LRIAS 1450
QY 341 LTMQYPEG-----YLEALANRERENSKREBEEOQEGGFASPRTGKWKWKRSAGGCP 394

Db 1451 RSTRHSHGLQADVFLVVELLSPRKRGRKSANNTPNSPNFNFRIATKSSEQRSVNI 1510
QY 395 S-----RAGSPRRTSKTKVPEYSLTAQOSS-----LIREDKSNA 429
Db 1511 ASKLSLOESKRRCKRQSPSPVTLGRSSRGQGVHLSAFEQLVVELVRHDDS-- 1568
QY 430 KLNVEVLASLKDPAAGSGPFQFLSKVETFCICQQLVFRPI-----TTVCQHN 481
Db 1569 --W-----PFLKLVSKI-----QVPDYDIKKPIALNIIREKVNKCEYKL 1607
QY 482 CKDCLD 487
Db 1608 ASEFID 1613

RESULT 8

US-09-839-479-69
; Sequence 69, Application US/09839479
; Patent No. 6727222
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 1673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-69

Query Match 5.1%; Score 149; DB 4; Length 1673;
Best Local Similarity 17.9%; Pred. No. 0.00017;
Matches 87; Conservative 60; Mismatches 145; Indels 194; Gaps 20;
QY 56 CHLCGRQDPDKQLMCDCEMFAHIYCLDPPILSSVPSDEWYCPCECRNDASEVVLAGERL 115
Db 1268 CKICRKKGAENMVLCDCDRGHHTYCVRPKLKIVP-EGDWFCPECR----- 1313
QY 116 RESKNAKMASATSSSQORDWKGMACVGRTECTIVPSNHYGPIGIPVGTWRRFRVQVS 175
Db 1314 --PKQRCRLS-----FR----- 1324
QY 176 ESGVHPHVAGIHGRSNDGSYSLVLAGVEDVDVHGNNFTYTGSGRDLSGNKRRTAEQSC 235
Db 1325 ----QRPSSLES-----DEDVEDSM-----GGBDDEVD-----GDEEGOSEEEYEV 1362
QY 236 DQKLTNTNRLALNCFAPINDQEGAEAKDWRSGKP-VRVVRNVKGGKNSKYAPAEGRYD 294
Db 1363 EQDEDS-----QEEEVSLPKGRQVRLPVKTRGKLSFSRQOQEP 1408
QY 295 GIYKVKVWPEK-----GKSGFLVMRYLLRRDDDEPGPWTKEGDKRIKLG 340
Db 1409 GR-----PSRSQOSTPKTTVSSKTGRS-----LRKINSAPPTETKS-----LRIAS 1450
QY 341 LTMQYPEG-----YLEALANRERENSKREBEEOQEGGFASPRTGKWKWKRSAGGCP 394
Db 1451 RSTRHSHGLQADVFLVVELLSPRKRGRKSANNTPNSPNFNFRIATKSSEQRSVNI 1510
QY 395 S-----RAGSPRRTSKTKVPEYSLTAQOSS-----LIREDKSNA 429
Db 1511 ASKLSLOESKRRCKRQSPSPVTLGRSSRGQGVHLSAFEQLVVELVRHDDS-- 1568

QY 430 KLWNEVLASLDRPASGSPQLFLSKVETTFQICQELVFRPI-----TTVCQHNV 481
Db 1569 --W-----PFLKLVSKI-----QVPDYDIIRKPIALNIIRKVNKCEYKL 1607
QY 482 CKDCLD 487
Db 1608 ASEFID 1613

RESULT 9
US-09-418-710-27
; Sequence 27, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-27

Query Match 5.1%; Score 147; DB 4; Length 1527;
Best Local Similarity 36.7%; Pred. No. 0.00022;
Matches 29; Conservative 13; Mismatches 29; Indels 8; Gaps 2;
QY 56 CHLCGRQDPDKQLMCDCEMFAHYICLDPLPSSVPSDEWYCPCECRNDASEVVLGERL 115
Db 1187 CKVCPKGGDDKLILCDECNKAFHLFCLRPALYVP-DGEWQCPACQP-----ATARR 1238
QY 116 RESKNAKMASATSSSQRD 134
Db 1239 NSRGRNYTEESASEDSED 1257

RESULT 10
US-09-839-479-27
; Sequence 27, Application US/09839479
; Patent No. 6727222
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-27

Query Match 5.1%; Score 147; DB 4; Length 1527;
Best Local Similarity 36.7%; Pred. No. 0.00022;
Matches 29; Conservative 13; Mismatches 29; Indels 8; Gaps 2;
QY 56 CHLCGRQDPDKQLMCDCEMFAHYICLDPLPSSVPSDEWYCPCECRNDASEVVLGERL 115
Db 1187 CKVCPKGGDDKLILCDECNKAFHLFCLRPALYVP-DGEWQCPACQP-----ATARR 1238
QY 116 RESKNAKMASATSSSQRD 134
Db 1239 NSRGRNYTEESASEDSED 1257

RESULT 11
US-09-418-710-29
; Sequence 29, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-29

Query Match 5.1%; Score 147; DB 4; Length 1531;
Best Local Similarity 36.7%; Pred. No. 0.00022;
Matches 29; Conservative 13; Mismatches 29; Indels 8; Gaps 2;
QY 56 CHLCGRQDPDKQLMCDCEMFAHYICLDPLPSSVPSDEWYCPCECRNDASEVVLGERL 115
Db 1191 CKVCPKGGDDKLILCDECNKAFHLFCLRPALYVP-DGEWQCPACQP-----ATARR 1242
QY 116 RESKNAKMASATSSSQRD 134
Db 1243 NSRGRNYTEESASEDSED 1261

RESULT 12
US-09-839-479-29
; Sequence 29, Application US/09839479
; Patent No. 6727222
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531
; TYPE: PRT
US-09-839-479-29

```

; ORGANISM: Homo sapiens
US-09-839-479-29

Query Match          5.1%; Score 147; DB 4; Length 1531;
Best Local Similarity 36.7%; Pred. No. 0.00022;
Matches 29; Conservative 13; Mismatches 29; Indels 8; Gaps 2;

QY 56 CHLCGGRRDPDKQLMCDCECMAFHIYCLDPLSSVPSEDEWYCPCRNDASEVWLAGRL 115
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1191 CKVCPKGGEDDKLILCDECNKAFHLFCLRPALYEVP-DGEWQCPACQP-----ATARR 1242
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 RESKKNKMASATSSSQRD 134
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1243 NSRGRNYTESASEDSD 1261
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-949-016-7037
; Sequence 7037, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7037
; LENGTH: 1540
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7037

Query Match          5.1%; Score 147; DB 4; Length 1540;
Best Local Similarity 36.7%; Pred. No. 0.00023;
Matches 29; Conservative 13; Mismatches 29; Indels 8; Gaps 2;

QY 56 CHLCGGRRDPDKQLMCDCECMAFHIYCLDPLSSVPSEDEWYCPCRNDASEVWLAGRL 115
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1244 CKVCRKGGEDDKLILCDECNKAFHLFCLRPALYEVP-DGEWQCPACQP-----ATARR 1295
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 RESKKNKMASATSSSQRD 134
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1296 NSRGRNYTESASEDSD 1314
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-09-538-092-1033
; Sequence 1033, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1033
; LENGTH: 1722

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 25, 2005, 16:38:02 ; Search time 166 Seconds
(without alignments)
1237.167 Million cell updates/sec

Title: US-10-019-071-2_COPY_263_793

Perfect score: 2896

Sequence: 1 DDLNDRIRIFVDFVKIER.....VNQPLQTVLNQLFPGYGNR 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2896	100.0	793	4	ABB76980	Human Inv	Abb76980 Human Inv
2	2887	99.7	793	6	ABR48157	Human bla	Abr48157 Human bla
3	2887	99.7	793	7	ADF61820	Human NP9	Adf61820 Human NP9
4	2887	99.7	793	7	ADF76781	Novel hum	Adf76781 Novel hum
5	2887	99.7	793	8	ADN05229	Antipsori	Adn05229 Antipsori
6	2887	99.7	793	8	ADO20357	Human PRO	Ado20357 Human PRO
7	2887	99.7	793	8	ADP55676	Human PRO	Adp55676 Human PRO
8	2815	97.2	780	6	ABU56628	Lung canc	Abu56628 Lung canc
9	2815	97.2	780	7	ADN38838	Cancer/an	Adn38838 Cancer/an
10	1718.5	59.3	802	6	ABR82238	Human nuc	Abr82238 Human nuc
11	1562	53.9	770	8	ABR83220	Human dia	Abm83220 Human dia
12	1297	44.8	645	6	ABU69599	Human NF-	Abu69599 Human NF-
13	1297	44.8	645	6	ABU69620	Human NF-	Abu69620 Human NF-
14	926	32.0	174	4	ABB76983	Human Inv	Abb76983 Human Inv
15	823.5	28.4	198	5	ABP64013	Human ORF	Abp64013 Human ORF
16	672	23.2	133	6	AAU16348	Human nov	Aau16348 Human nov
17	672	23.2	133	6	ABU55417	Human nov	Abu55417 Human nov
18	588.5	20.3	617	7	ADD30490	Plant tra	Add30490 Plant tra
19	588.5	20.3	617	8	ADI43851	Plant tra	Adi43851 Plant tra
20	428.5	14.8	233	3	AAB42314	Human ORF	Aab42314 Human ORF
21	420.5	14.5	178	4	AAU16350	Human nov	Aau16350 Human nov
22	420.5	14.5	178	6	ABU55419	Human nov	Abu55419 Human nov
23	420.5	14.5	180	4	AAU42002	Human pol	Aau42002 Human pol
24	357.5	12.3	110	4	AAU15895	Human nov	Aau15895 Human nov
25	357.5	12.3	110	6	ABU54964	Human nov	Abu54964 Human nov

26	287	9.9	71	4	AAW40216	Human pol	Aam40216 Human pol
27	287	9.9	71	4	AAW73737	Ring fing	Aab73737 Ring fing
28	263	9.1	781	3	AAG32044	Arabidops	Aag32044 Arabidops
29	263	9.1	785	3	AAG32043	Arabidops	Aag32043 Arabidops
30	263	9.1	788	3	AAG32042	Arabidops	Aag32042 Arabidops
31	247	8.5	89	4	AAO07182	Human pol	Aao07182 Human pol
32	235.5	8.1	670	8	ADN72155	Thale cre	Adn72155 Thale cre
33	235.5	8.1	1072	3	AAG41664	Arabidops	Aag41664 Arabidops
34	235.5	8.1	1079	3	AAG41663	Arabidops	Aag41663 Arabidops
35	235.5	8.1	1132	3	AAG41662	Arabidops	Aag41662 Arabidops
36	229.5	7.9	856	8	ADM48182	Polypepti	Adm48182 Polypepti
37	190	6.6	87	5	ABN97911	Human sec	Abn97911 Human sec
38	186.5	6.4	1398	5	ABG97491	Human NOV	Abg97491 Human NOV
39	186.5	6.4	1400	4	ABR83348	AAP-2 pro	Aab83348 AAP-2 pro
40	186.5	6.4	1445	6	ABR41365	Human DIT	AbR41365 Human DIT
41	180.5	6.2	2897	4	ABR58514	Drosophil	AbR58514 Drosophil
42	177	6.1	4019	4	AAE13839	Human lun	Aae13839 Human lun
43	177	6.1	4019	7	ADD66733	Human lun	Add66733 Human lun
44	177	6.1	4019	7	ADE87987	Human lun	Ade87987 Human lun
45	177	6.1	4025	5	ABP69736	Human pol	Abp69736 Human pol

ALIGNMENTS

RESULT 1
ABB76980
ID ABB76980 standard; protein; 793 AA.
XX
AC ABB76980;
XX
DT 22-JUL-2002 (first entry)
XX
DE Human Inverted CCAAT box binding protein, ICBP90.
XX
KW Human; inverted CCAAT box binding protein; ICBP90; cytosolic;
KW cell proliferation control; inverted CCAAT box; cancer.
XX
OS Homo sapiens.
XX
PN WO200078949-A1.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-2000; 2000WO-FR001747.
XX
PR 22-JUN-1999; 99FR-00007935.
XX
(ADBR-) ADEREGEM ASSOC DEV RECH EN GENETIQ.
XX
PI Bronner C, Hopfner R, Mousli M, Jeltsch J, Lutz Y, Oudet P;
XX
DR WPI; 2001-091571/10.
DR N-PSDB; ABL58020.
XX
PT Novel inverted CCAAT box binding protein, and related nucleic acids,
PT antibodies and specific ligands, useful for treating and preventing
PT cancer.
XX
PS Claim 1; Fig 7; 115pp; French.
XX
CC The present sequence is the protein sequence for human ICBP90 (inverted
CC CCAAT box binding protein). The inverted CCAAT box is implicated in cell
CC proliferation control. Several copies of the inverted CCAAT box are
CC present in the promoter of the topoisomerase IIalpha gene, and also
CC functions as a nuclear receptor. ICBP90 and its coding sequence are
CC useful for treatment and/or prevention of cancer
SQ
Sequence 793 AA;

Query Match 100.0%; Score 2896; DB 4; Length 793;
Best Local Similarity 100.0%; Pred. No. 2.6e-257;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 DDLNDLCRIIFVDEVPKIERPBGSGPMVDNPMRRKSGPSCXKCKDQVNLRCVCAHLGG 60
Db |||
QY 263 DDLNDLCRIIFVDEVPKIERPBGSGPMVDNPMRRKSGPSCXKCKDQVNLRCVCAHLGG 322
Db |||
QY 61 GRQDPDKQLMCDCECDMAFHYICLDPPLSSVPSEDEWYCPCRNDASEVVLAGERLRESKK 120
Db |||
QY 323 GRQDPDKQLMCDCECDMAFHYICLDPPLSSVPSEDEWYCPCRNDASEVVLAGERLRESKK 382
Db |||
QY 121 NAKMASATSSSQORDMGKMACVGRTEKCTIVPSNHYGPIPGIPVGTMMRFRVQVSEGVH 180
Db |||
QY 383 NAKMASATSSSQORDMGKMACVGRTEKCTIVPSNHYGPIPGIPVGTMMRFRVQVSEGVH 442
QY 181 RPHVAGIHGRSNDGYSVLVLAGYEDVDHGNFFYTGSGGRDLSGNKRRTABQSCDQKLT 240
Db |||
QY 443 RPHVAGIHGRSNDGYSVLVLAGYEDVDHGNFFYTGSGGRDLSGNKRRTABQSCDQKLT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRNVKGGKNSKYAPAEGRYDGIYKV 300
Db |||
QY 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRNVKGGKNSKYAPAEGRYDGIYKV 562
QY 301 KYWPEKSGGLVWRYLLRRDDDEPGPWTKEGKDRICKLGLTMQYPEGYLEALANREREK 360
Db |||
QY 563 KYWPEKSGGLVWRYLLRRDDDEPGPWTKEGKDRICKLGLTMQYPEGYLEALANREREK 622
QY 361 ENSKREEBEQEGGFASPTGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 420
Db |||
QY 623 ENSKREEBEQEGGFASPTGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 682
QY 421 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFQICCCQELVFRPITTVCOHN 480
Db |||
QY 683 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFQICCCQELVFRPITTVCOHN 742
QY 481 VKDCCLDRSFRAQVFCSPACRYDLGRSYAMQVNPQLQTVLNLQFPYGNNGR 531
Db |||
QY 743 VKDCCLDRSFRAQVFCSPACRYDLGRSYAMQVNPQLQTVLNLQFPYGNNGR 793
Db |||

RESULT 2
ABR48157
ID ABR48157 standard; protein; 793 AA.
AC ABR48157;
XX
XX 12-JUN-2003 (first entry)
XX
XX Human bladder cancer associated protein sequence SEQ ID NO:27.
XX
XX Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO2003003906-A2.
XX
XX 16-JAN-2003.
XX
XX 03-JUL-2002; 2002WO-US021338.
XX
XX 03-JUL-2001; 2001US-0302814P.
XX
XX 03-AUG-2001; 2001US-0310099P.
XX
XX 08-NOV-2001; 2001US-0343705P.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX
XX 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Mack DH, Aziz N;
XX
XX WPI; 2003-201532/19.
XX
XX N-PSDB; ACC50965.
XX
XX Detecting a bladder cancer-associated transcript in a cell from a
XX patient, comprises contacting a biological sample from the patient with a
```

```
PT bladder cancer-associated polynucleotide or antibody.
XX Claim 10; Page 238; 307pp; English.
PS
XX The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridises to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
XX
XX Sequence 793 AA;
SQ
Query Match 99.7%; Score 2887; DB 6; Length 793;
Best Local Similarity 99.6%; Pred. No. 1.8e-256;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDLNDLCRIIFVDEVPKIERPBGSGPMVDNPMRRKSGPSCXKCKDQVNLRCVCAHLGG 60
Db |||
QY 263 DDLNDLCRIIFVDEVPKIERPBGSGPMVDNPMRRKSGPSCXKCKDQVNLRCVCAHLGG 322
Db |||
QY 61 GRQDPDKQLMCDCECDMAFHYICLDPPLSSVPSEDEWYCPCRNDASEVVLAGERLRESKK 120
Db |||
QY 323 GRQDPDKQLMCDCECDMAFHYICLDPPLSSVPSEDEWYCPCRNDASEVVLAGERLRESKK 382
QY 121 NAKMASATSSSQORDMGKMACVGRTEKCTIVPSNHYGPIPGIPVGTMMRFRVQVSEGVH 180
Db |||
QY 383 NAKMASATSSSQORDMGKMACVGRTEKCTIVPSNHYGPIPGIPVGTMMRFRVQVSEGVH 442
QY 181 RPHVAGIHGRSNDGYSVLVLAGYEDVDHGNFFYTGSGGRDLSGNKRRTABQSCDQKLT 240
Db |||
QY 443 RPHVAGIHGRSNDGYSVLVLAGYEDVDHGNFFYTGSGGRDLSGNKRRTABQSCDQKLT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRNVKGGKNSKYAPAEGRYDGIYKV 300
Db |||
QY 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRNVKGGKNSKYAPAEGRYDGIYKV 562
QY 301 KYWPEKSGGLVWRYLLRRDDDEPGPWTKEGKDRICKLGLTMQYPEGYLEALANREREK 360
Db |||
QY 563 KYWPEKSGGLVWRYLLRRDDDEPGPWTKEGKDRICKLGLTMQYPEGYLEALANREREK 622
QY 361 ENSKREEBEQEGGFASPTGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 420
Db |||
QY 623 ENSKREEBEQEGGFASPTGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 682
QY 421 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFQICCCQELVFRPITTVCOHN 480
Db |||
QY 683 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFQICCCQELVFRPITTVCOHN 742
QY 481 VKDCCLDRSFRAQVFCSPACRYDLGRSYAMQVNPQLQTVLNLQFPYGNNGR 531
Db |||
QY 743 VKDCCLDRSFRAQVFCSPACRYDLGRSYAMQVNPQLQTVLNLQFPYGNNGR 793
Db |||

RESULT 3
ADF61820
ID ADF61820 standard; protein; 793 AA.
XX
XX ADF61820;
AC ADF61820;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human NP95 protein.
XX
```

KW cell cycle arrest; cytostatic; antipsoriatic; antiarteriosclerotic;
KW vasotropic; antithyroid; melanoma; breast; ovarian; lung;
KW gastrointestinal; colon cancer; Grave's disease; psoriasis;
KW atherosclerosis; restenosis; vasoproliferative; human; NP95.
XX Homo sapiens.
XX WO2003088910-A2.
XX 30-OCT-2003.
XX 15-APR-2003; 2003WO-US011867.
XX 15-APR-2002; 2002US-00123569.
XX 15-APR-2002; 2002US-00123731.
XX 16-APR-2002; 2002US-0373366P.
XX (RIGE-) RIGEL PHARM INC.
XX Hitoshi Y, Jenkins Y;
XX WPI: 2003-865396/80.
XX N-PSDB; ADF61819.
XX Identifying a compound that modulates cell cycle arrest, for treating
PT e.g. cancer, comprises contacting a cell comprising a target polypeptide
PT and determining the chemical or phenotypic effect of the compound upon
PT the cell.
XX Claim 1; SEQ ID NO 4; 176pp; English.
XX The invention relates to a novel method for identifying a compound that
CC modulates cell cycle arrest comprising contacting a target polypeptide
CC within a cell with a compound and determining the chemical or phenotypic
CC effect of the compound upon the cell. The method of the invention has
CC cytostatic, antipsoriatic, antiarteriosclerotic, vasotropic and
CC antithyroid applications and may be useful for identifying a compound
CC that modulates cell cycle arrest. Such compounds may subsequently be used
CC for developing therapeutic reagents to treat melanoma, breast, ovarian,
CC lung, gastrointestinal or colon cancer, as well as other proliferative,
CC diseases such as Grave's disease, psoriasis, atherosclerosis, restenosis
CC and other vasoproliferative diseases. The current sequence is that of the
CC human NP95 protein of the invention.
XX Sequence 793 AA;
SQ
Query Match 99.7%; Score 2887; DB 7; Length 793;
Best Local Similarity 99.6%; Pred. No. 1.8e-256;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDLNDCRIIFVDEVPKIERPGEKSPVMDNPMRRKSGPSCKCKDDVNLRCVACHLCG 60
DB 263 DDLNDCRIIFVDEVPKIERPGEKSPVMDNPMRRKSGPSCKCKDDVNLRCVACHLCG 322
QY 61 GRQDPDKQLMCDCEMAFHYICLDPLSSVPSEDEWYCEPCRDASEVVLAGERLRESKK 120
DB 323 GRQDPDKQLMCDCEMAFHYICLDPLSSVPSEDEWYCEPCRDASEVVLAGERLRESKK 382
QY 121 NAKMASATSSQSDWKGMACVGRTEKCTIVPSNHYGPIPGIPVGMWFRVQVSESGVH 180
DB 383 KAKMASATSSQSDWKGMACVGRTEKCTIVPSNHYGPIPGIPVGMWFRVQVSESGVH 442
QY 181 RPHVAGIHRSDNGSVLVLGGYEDVDHGFNFTYTGSGGRDLSNKKETAQSCDCKLT 240
DB 443 RPHVAGIHRSDNGSVLVLGGYEDVDHGFNFTYTGSGGRDLSNKKETAQSCDCKLT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNVKGGKSKYAPAGNRYDGIYKV 300
DB 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNVKGGKSKYAPAGNRYDGIYKV 562
QY 301 KYWPEKSGFLVWRYLLRRDDDEPGPWTKEGKNDRIKKLGLTMQYPEGYLEALANREK 360
DB 563 KYWPEKSGFLVWRYLLRRDDDEPGPWTKEGKNDRIKKLGLTMQYPEGYLEALANREK 622

QY 361 ENSKREEEQEGGFAGPRTCKGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 420
DB 623 ENSKREEEQEGGFAGPRTCKGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 682
QY 421 LIREDKSNAKLWNEVLASLDRPASGSPFQLFLSKVETFCICCOELVFRPITTVCCOHN 480
DB 683 LIREDKSNAKLWNEVLASLDRPASGSPFQLFLSKVETFCICCOELVFRPITTVCCOHN 742
QY 481 VKDCLDRSFRAQVFSFPCRYDLSRSYAMQVNPLOTVLNQLPFGYNGR 531
DB 743 VKDCLDRSFRAQVFSFPCRYDLSRSYAMQVNPLOTVLNQLPFGYNGR 793

RESULT 4

ADF76781
ID ADF76781 standard; protein; 793 AA.

XX ADF76781;

XX 26-FEB-2004 (first entry)

XX Novel human secreted and transmembrane protein SeqID 456.

XX human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.

XX Homo sapiens.

XX WO2003072035-A2.

XX 04-SEP-2003.

XX 21-FEB-2003; 2003WO-US005241.

XX 22-FEB-2002; 2002US-0359461P.

XX (GETH) GENENTECH INC.

XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;

XX WPI: 2003-721702/68.

XX N-PSDB; ADF76780.

XX New PRO polypeptides, useful for diagnosing and treating an immune
PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
PT diabetes mellitus.

PS Claim 10; SEQ ID NO 456; 918pp; English.

XX This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or

CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
CC invention.

XX
SQ Sequence 793 AA;
Query Match 99.7%; Score 2887; DB 7; Length 793;
Best Local Similarity 99.6%; Pred. No. 1.8e-256;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDLNDLCRIIFVDEVKIERPGEKSPMDNPMRRKSGPSCKHCKDDVNLRCRVCAHLCG 60
DB DDLNDLCRIIFVDEVKIERPGEKSPMDNPMRRKSGPSCKHCKDDVNLRCRVCAHLCG 322
QY 61 GRQDPDKQLMCDCECMAFHIYCLDPLSSVPSEDEWYCEPCRNDAEVLVLAGERLRESKK 120
DB GRQDPDKQLMCDCECMAFHIYCLDPLSSVPSEDEWYCEPCRNDAEVLVLAGERLRESKK 382
QY 121 NAKMASATSSORDMGKGMACVGRTECTIVPSNHYGPIPGIPVGTMMRFVQVSESGVH 180
DB KAKMASATSSORDMGKGMACVGRTECTIVPSNHYGPIPGIPVGTMMRFVQVSESGVH 442
QY 181 RPHVAGIHGRSNDGAYSLVLAGGYEDDVGHNFFYTGSGGRDLGSKNKTAEQSCDQKLT 240
DB RPHVAGIHGRSNDGAYSLVLAGGYEDDVGHNFFYTGSGGRDLGSKNKTAEQSCDQKLT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRYDGIYKV 300
DB NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRYDGIYKV 562
QY 301 KYWPEKSGSGLVWRYLLRRDDDEPGWTKGKDRICKLGLTMQYPEGYLEALANREREK 360
DB KYWPEKSGSGLVWRYLLRRDDDEPGWTKGKDRICKLGLTMQYPEGYLEALANREREK 622
QY 361 ENSKREEEQEGGFASPRGKWKRSAGGSPRAGSPRRTSKTKVEPYSLTAQSS 420
DB ENSKREEEQEGGFASPRGKWKRSAGGSPRAGSPRRTSKTKVEPYSLTAQSS 682
QY 421 LIREDKSNAKLWNEVLASLKDPSGSPFQLFLSKVEETFCICQELVFRPITTVCOHN 480
DB LIREDKSNAKLWNEVLASLKDPSGSPFQLFLSKVEETFCICQELVFRPITTVCOHN 742
QY 481 VCKDCLDRSFRAQVFCPCACRYDLGRSYAMOVNQLQTLVNLQFPYGNR 531
DB VCKDCLDRSFRAQVFCPCACRYDLGRSYAMOVNQLQTLVNLQFPYGNR 793

RESULT 5

ADN05229
ID ADN05229 standard; protein; 793 AA.
XX
AC ADN05229;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic protein sequence #791.
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
XX Homo sapiens.
XX
XX WO2004028479-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030907.
XX
XX 25-SEP-2002; 2002US-0414006P.
XX
XX (GETH) GENENTECH INC.
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;

XX
DR WPI; 2004-305105/28.
XX N-PSDB; ADN05228.

XX
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.

PS Claim 9; SEQ ID NO 1623; 3069pp; English.

XX
CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

XX
SQ Sequence 793 AA;

Query Match 99.7%; Score 2887; DB 8; Length 793;
Best Local Similarity 99.6%; Pred. No. 1.8e-256;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDLNDLCRIIFVDEVKIERPGEKSPMDNPMRRKSGPSCKHCKDDVNLRCRVCAHLCG 60
DB DDLNDLCRIIFVDEVKIERPGEKSPMDNPMRRKSGPSCKHCKDDVNLRCRVCAHLCG 322
QY 61 GRQDPDKQLMCDCECMAFHIYCLDPLSSVPSEDEWYCEPCRNDAEVLVLAGERLRESKK 120
DB GRQDPDKQLMCDCECMAFHIYCLDPLSSVPSEDEWYCEPCRNDAEVLVLAGERLRESKK 382
QY 121 NAKMASATSSORDMGKGMACVGRTECTIVPSNHYGPIPGIPVGTMMRFVQVSESGVH 180
DB KAKMASATSSORDMGKGMACVGRTECTIVPSNHYGPIPGIPVGTMMRFVQVSESGVH 442
QY 181 RPHVAGIHGRSNDGAYSLVLAGGYEDDVGHNFFYTGSGGRDLGSKNKTAEQSCDQKLT 240
DB RPHVAGIHGRSNDGAYSLVLAGGYEDDVGHNFFYTGSGGRDLGSKNKTAEQSCDQKLT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRYDGIYKV 300
DB NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRYDGIYKV 562
QY 301 KYWPEKSGSGLVWRYLLRRDDDEPGWTKGKDRICKLGLTMQYPEGYLEALANREREK 360
DB KYWPEKSGSGLVWRYLLRRDDDEPGWTKGKDRICKLGLTMQYPEGYLEALANREREK 622
QY 361 ENSKREEEQEGGFASPRGKWKRSAGGSPRAGSPRRTSKTKVEPYSLTAQSS 420
DB ENSKREEEQEGGFASPRGKWKRSAGGSPRAGSPRRTSKTKVEPYSLTAQSS 682
QY 421 LIREDKSNAKLWNEVLASLKDPSGSPFQLFLSKVEETFCICQELVFRPITTVCOHN 480
DB LIREDKSNAKLWNEVLASLKDPSGSPFQLFLSKVEETFCICQELVFRPITTVCOHN 742
QY 481 VCKDCLDRSFRAQVFCPCACRYDLGRSYAMOVNQLQTLVNLQFPYGNR 531
DB VCKDCLDRSFRAQVFCPCACRYDLGRSYAMOVNQLQTLVNLQFPYGNR 793

RESULT 6

ADO20357
ID ADO20357 standard; protein; 793 AA.
XX
AC ADO20357;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #626.

XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;

KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX Homo sapiens.
PN WO2004043361-A2.
XX 27-MAY-2004.
XX 06-NOV-2003; 2003WO-US035268.
XX 08-NOV-2002; 2002US-0425235P.
XX (GETH) GENENTECH INC.
XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX WPI; 2004-420067/39.
DR N-PSDB; ADO20356.
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX Claim 7; SEQ ID NO 1252; 173lpp; English.
XX The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
XX invention.
SQ Sequence 793 AA;
Query Match 99.7%; Score 2887; DB 8; Length 793;
Best Local Similarity 99.6%; Pred. No. 1.8e-256;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDLNDCRIIFVDEVFKIERPGSGSPWVDNPMRKRKSGPSCKCKDDVNRLCRVACHLCG 60
DB 263 DDLNDCRIIFVDEVFKIERPGSGSPWVDNPMRKRKSGPSCKCKDDVNRLCRVACHLCG 322
QY 61 GRQDPKQLMCDCECDMAFYICLDPLPSSVPSDEWYCPBCRNDAEVLVLAGERLESKK 120
DB 323 GRQDPKQLMCDCECDMAFYICLDPLPSSVPSDEWYCPBCRNDAEVLVLAGERLESKK 382
QY 121 NAKMASATSSQRDWGKGMACVGRTECTIVPSNHYGPIPGIPVGTWMPFRVQVSSGVH 180
DB 383 KAKMASATSSQRDWGKGMACVGRTECTIVPSNHYGPIPGIPVGTWMPFRVQVSSGVH 442
QY 181 RPHVAGTHGSHDGSYSLVLAGVEDDDVHGNEFTYTGSGRDLGKRTAEQSCDQKLT 240
DB 443 RPHVAGTHGSHDGSYSLVLAGVEDDDVHGNEFTYTGSGRDLGKRTAEQSCDQKLT 502
QY 241 NTRALALNCFAPINDOEGAEAKDWRSGKFPVRVVRNVKGGNSKYAPAEGRNRYDGIYKV 300
DB 503 NTRALALNCFAPINDOEGAEAKDWRSGKFPVRVVRNVKGGNSKYAPAEGRNRYDGIYKV 562
QY 301 KYWPEKSGFLVWRYLLRRDDDEPGWTKGKDRICKLGLTWQYEGYLEALANREK 360
DB 563 KYWPEKSGFLVWRYLLRRDDDEPGWTKGKDRICKLGLTWQYEGYLEALANREK 622

QY 361 ENSKREEEQEGGFPASPRTKGKWKRSAGGSPSRAGSPRRTSKTKVPSYSLTAQOSS 420
DB 623 ENSKREEEQEGGFPASPRTKGKWKRSAGGSPSRAGSPRRTSKTKVPSYSLTAQOSS 682
QY 421 LIREDKSNAKLWNEVLASLKDORPASGSPFOLFLSKVETFOCICQELVFRITTVCOHN 480
DB 683 LIREDKSNAKLWNEVLASLKDORPASGSPFOLFLSKVETFOCICQELVFRITTVCOHN 742
QY 481 VCKOCLDRSFRAQVFCPCACRYDLGRSYAMQVNPQLQTVLNLQFFGYNGR 531
DB 743 VCKOCLDRSFRAQVFCPCACRYDLGRSYAMQVNPQLQTVLNLQFFGYNGR 793
RESULT 7
ADP55676
ID ADP55676 standard; protein; 793 AA.
XX
AC ADP55676;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human PRO protein sequence SEQ ID NO:1652.
XX
KW human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW virucide; gene therapy.
XX
OS Homo sapiens.
XX WO2004039956-A2.
XX 13-MAY-2004.
XX 28-OCT-2003; 2003WO-US034381.
XX 29-OCT-2002; 2002US-0422472P.
XX (GETH) GENENTECH INC.
XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX WPI; 2004-376182/35.
DR N-PSDB; ADP55675.
XX
PT New PRO polynucleotides and polypeptides, useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.
XX
PS Claim 1; SEQ ID NO 1652; 3009pp; English.
XX
CC The present invention describes an isolated PRO nucleic acid (1). Also
CC described: (1) a vector comprising (1); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptide; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC ; and (13) a method of stimulating the immune response in a mammal. The

CC PRO sequences have antiallergic, antianaemic, antiarthritic,
CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,
CC antirheumatic, antithyroid, CNS, dermatological, immunosuppressive, muscular,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (I) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO protein from the present invention.
XX
SQ Sequence 793 AA;

Query Match 99.7%; Score 2887; DB 8; Length 793;
Best Local Similarity 99.6%; Pred. No. 1.8e-256;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDSLNDCRIIFVDEVFKEIRPGEPSMVDNPMRRKSGPSCKHCKDQVNRNLCRCVACHLCG 60
Db DDSLNDCRIIFVDEVFKEIRPGEPSMVDNPMRRKSGPSCKHCKDQVNRNLCRCVACHLCG 322
QY 61 GRQDPDKQLMCDCECDMAFHICYLDPPLSSVPEDEWYCEPCNDASEVVLAGERLRESKK 120
Db GRQDPDKQLMCDCECDMAFHICYLDPPLSSVPEDEWYCEPCNDASEVVLAGERLRESKK 382
QY 121 NAKMASATSSORDWKGKMACVGRKTECTIVPSNHYGPIPGIPVGTMMRFRVQVSEGVH 180
Db 383 KAKMASATSSORDWKGKMACVGRKTECTIVPSNHYGPIPGIPVGTMMRFRVQVSEGVH 442
QY 181 RPHVAGIHGRSNDGYSYLVLAGGYEDVDHGNFFTYTSGGRDLGSGNKRKTABQSCDQKLT 240
Db 443 RPHVAGIHGRSNDGYSYLVLAGGYEDVDHGNFFTYTSGGRDLGSGNKRKTABQSCDQKLT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVNGGKNSKYAPAGNRYDGIYKV 300
Db 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVNGGKNSKYAPAGNRYDGIYKV 562
QY 301 KYWPEKSGGFLVWYLLRRDDPGFWTKGKDRICKLGLTMQYPEGYLEALANRERK 360
Db 563 KYWPEKSGGFLVWYLLRRDDPGFWTKGKDRICKLGLTMQYPEGYLEALANRERK 622
QY 361 ENSKREEEQOEGGFASPTGKWKRSAGGSPRSGSAGGSPRSTKTKVEPSYSLTAQSS 420
Db 623 ENSKREEEQOEGGFASPTGKWKRSAGGSPRSGSAGGSPRSTKTKVEPSYSLTAQSS 682
QY 421 LIREDKSNAKLMNEVLASLKDPSAGSPFQFLSKVEETFCICCOELVFRPITTVCOHN 480
Db 683 LIREDKSNAKLMNEVLASLKDPSAGSPFQFLSKVEETFCICCOELVFRPITTVCOHN 742
QY 481 VKDCLDLDRFRAQVFCPCRYDLGRSYAMQVNOPLQTLNOLFPQYGNR 531
Db 743 VKDCLDLDRFRAQVFCPCRYDLGRSYAMQVNOPLQTLNOLFPQYGNR 793

RESULT 8
ABU56628
ID ABU56628 standard; protein; 780 AA.
XX
AC ABU56628;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #21.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.

XX 31-OCT-2002.
XX 18-APR-2002; 2002WO-US012476.
XX 18-APR-2001; 2001US-0284770P.
XX 10-MAY-2001; 2001US-0290492P.
XX 09-NOV-2001; 2001US-0339245P.
XX 13-NOV-2001; 2001US-0350668P.
XX 29-NOV-2001; 2001US-0334370P.
XX 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
XX WPI; 2003-093161/08.
XX N-PSDB; ABX76357.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX
XX Claim 27; Page 357; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridises
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, and
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
XX invention
XX
SQ Sequence 780 AA;
Query Match 97.2%; Score 2815; DB 6; Length 780;
Best Local Similarity 99.6%; Pred. No. 7.6e-250;
Matches 516; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDSLNDCRIIFVDEVFKEIRPGEPSMVDNPMRRKSGPSCKHCKDQVNRNLCRCVACHLCG 60
Db 263 DDSLNDCRIIFVDEVFKEIRPGEPSMVDNPMRRKSGPSCKHCKDQVNRNLCRCVACHLCG 322
QY 61 GRQDPDKQLMCDCECDMAFHICYLDPPLSSVPEDEWYCEPCNDASEVVLAGERLRESKK 120
Db 323 GRQDPDKQLMCDCECDMAFHICYLDPPLSSVPEDEWYCEPCNDASEVVLAGERLRESKK 382
QY 121 NAKMASATSSORDWKGKMACVGRKTECTIVPSNHYGPIPGIPVGTMMRFRVQVSEGVH 180
Db 383 KAKMASATSSORDWKGKMACVGRKTECTIVPSNHYGPIPGIPVGTMMRFRVQVSEGVH 442
QY 181 RPHVAGIHGRSNDGYSYLVLAGGYEDVDHGNFFTYTSGGRDLGSGNKRKTABQSCDQKLT 240
Db 443 RPHVAGIHGRSNDGYSYLVLAGGYEDVDHGNFFTYTSGGRDLGSGNKRKTABQSCDQKLT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVNGGKNSKYAPAGNRYDGIYKV 300
Db 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVNGGKNSKYAPAGNRYDGIYKV 562
QY 301 KYWPEKSGGFLVWYLLRRDDPGFWTKGKDRICKLGLTMQYPEGYLEALANRERK 360

Db 563 KTWPEKSGFLVWRYLLRRDDDEPGPWTKEGDKRIKGLTQWYPEGYLEALANRREK 622
QY 361 ENSKREEEQEGGFASPRGTGKWKRSAGGSPRAGSPRTSKTKVPEYSLTAQSS 420
Db 623 ENSKREEEQEGGFASPRGTGKWKRSAGGSPRAGSPRTSKTKVPEYSLTAQSS 682
QY 421 LIREDKSNKLNWVLSLKDPRASGSPQLFLSKVEETFCICQELVFRPITTVCOHN 480
Db 683 LIREDKSNKLNWVLSLKDPRASGSPQLFLSKVEETFCICQELVFRPITTVCOHN 742
QY 481 VKCDLDRSFRAQVFCPCRYDLGRSYAMQVNOPLQT 518
Db 743 VKCDLDRSFRAQVFCPCRYDLGRSYAMQVNOPLQT 780
RESULT 9
ADN38838
ID ADN38838 standard; protein; 780 AA.
XX
AC ADN38838;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:156.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnary; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX WO2003042661-A2.
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KB, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR N-PSDB; ADN38837.
XX
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX

PS Claim 12; SEQ ID NO 156; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 780 AA;
Query Match 97.2%; Score 2815; DB 7; Length 780;
Best Local Similarity 99.6%; Pred. No. 7.6e-250;
Matches 516; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDSLNDCHRIIFVDEVFKIERPGEPSMVDNPMRRKSGPSCKHCKDDVNLRCVACHLCG 60
Db 263 DDSLNDCHRIIFVDEVFKIERPGEPSMVDNPMRRKSGPSCKHCKDDVNLRCVACHLCG 322
QY 61 GRQDPDKQLMDECDMAFHIVCLDPLSSVPSDESWYCEPCNDASEVVLAGERLRESKK 120
Db 323 GRQDPDKQLMDECDMAFHIVCLDPLSSVPSDESWYCEPCNDASEVVLAGERLRESKK 382
QY 121 NAKMASATSSQORDMGKMACVGRTECTIVPSNHYGPIGIPVCTMRFRVQVSESGVH 180
Db 383 KAKMASATSSQORDMGKMACVGRTECTIVPSNHYGPIGIPVCTMRFRVQVSESGVH 442
QY 181 RPHVAGIHGRSNDGSYSLVLAGGYDDVDHGNFFYTGSGGRDLSGNKRTAQSCDQKIT 240
Db 443 RPHVAGIHGRSNDGSYSLVLAGGYDDVDHGNFFYTGSGGRDLSGNKRTAQSCDQKIT 502
QY 241 NTNRLALNCFAPINDQEGABAKWRSCKPVRVVRNVKGNKSKYAPAEGRNYDGIYKV 300
Db 503 NTNRLALNCFAPINDQEGABAKWRSCKPVRVVRNVKGNKSKYAPAEGRNYDGIYKV 562
QY 301 KYWPEKSGFLVWRYLLRRDDDEPGPWTKEGDKRIKGLTQWYPEGYLEALANRREK 360
Db 563 KYWPEKSGFLVWRYLLRRDDDEPGPWTKEGDKRIKGLTQWYPEGYLEALANRREK 622
QY 361 ENSKREEEQEGGFASPRGTGKWKRSAGGSPRAGSPRTSKTKVPEYSLTAQSS 420
Db 623 ENSKREEEQEGGFASPRGTGKWKRSAGGSPRAGSPRTSKTKVPEYSLTAQSS 682
QY 421 LIREDKSNKLNWVLSLKDPRASGSPQLFLSKVEETFCICQELVFRPITTVCOHN 480
Db 683 LIREDKSNKLNWVLSLKDPRASGSPQLFLSKVEETFCICQELVFRPITTVCOHN 742
QY 481 VKCDLDRSFRAQVFCPCRYDLGRSYAMQVNOPLQT 518
Db 743 VKCDLDRSFRAQVFCPCRYDLGRSYAMQVNOPLQT 780
RESULT 10
ABR82238
ID ABR82238 standard; protein; 802 AA.
XX
AC ABR82238;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human nucleic acid-associated protein (NAAP)-Id 4706628CD1.
XX

KW NAAP; nucleic acid-associated protein; cardiant; cytostatic; transgenic;
KW neuroprotective; gene therapy; human; cancer.
XX Homo sapiens.
OS WO2003052048-A2.
PN 26-JUN-2003.
XX 02-MAY-2002; 2002WO-US014276.
XX 04-MAY-2001; 2001US-0288598P.
PR 17-MAY-2001; 2001US-0291776P.
PR 18-MAY-2001; 2001US-0292172P.
PR 25-MAY-2001; 2001US-0293564P.
XX (INCY-) INCYTE GENOMICS INC.
PA Yue H, Ding L, Baughn MR, Lal PG, Yue H, Hafalia AJA, Lee EA;
PI Ison CH, Becha SP, Gururajan R, Emerling BM, Griffin JA, Tang YT;
PI Lu DM, Yao MG, Chawla NK, Ramkumar J, Gandhi AK, Lee SY;
PI Richardson TW, Yang J, Elliott VS, Lu Y, Thangavelu K, He A;
PI Azimzai Y, Raumann BE, Swarnakar A, Burford N;
XX WPI: 2003-541640/51.
DR N-PSDB; ACP35646.
XX New human nucleic acid-associated proteins polypeptide, useful for
PT preparing a composition for diagnosing or treating e.g., cardiovascular
PT or neurological disorders.
XX Claim 1; Page 168-169; 212pp; English.
XX The invention relates to human nucleic acid-associated proteins (NAAP)
CC and encoding polynucleotides. The NAAP polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides are useful for
CC preparing a composition for diagnosing or treating a disease or condition
CC associated with decreased expression or overexpression of functional NAAP
CC e.g., cardiovascular or neurological disorders or cancer. The present
CC sequence represents a human NAAP polypeptide
XX Sequence 802 AA;
SQ
Query Match 59.3%; Score 1718.5; DB 6; Length 802;
Best Local Similarity 59.3%; Pred. No. 9.7e-149;
Matches 316; Conservative 77; Mismatches 116; Indels 25; Gaps 6;
QY 1 DDLNDICRIIFVDEVEFKIERPGEKSPM--VDNPMRKSGPCKCKDNDVNRICRVCAH 58
DB 291 EGTLDNCKIIISVDEIFKIERPG-AHPLSPADGKFLRNDPCDLCGGDEPKKCHSCSRV 349
QY 59 CGGRQDPDKQLMDECDMAFIYCLDPLSSVPSDEWYCPICRNDASVVLAGERLRS 118
DB 350 CGGKEHPNQLLDCENVAHYIYCLNPLDKVPEEYVYCPSCKTDSSSEVWAGERLKM 409
QY 119 KNAKMASATSSORDWGMGACVGTKECTIVPSNHYGPIPIGIVGTWRRVQVSESG 178
DB 410 KKAARPSASTSRRDWRGMGACVGTRECTIVPSNHYGPIPIGIVGTWRRVQVSEAG 469
QY 179 VHRPHVAGIHGRSNDGYSILVLAGGYEDVDHGNFTYTGSGRDLSGNKRRTAESCDQK 238
DB 470 VHRPHVGGIHGRSNDGAYSLVLAGGFADVDGDEFTYTGSGKNLAGNKRIGASADOT 529
QY 239 LTNTRALALNCFAPINDQGEAFADKWRSGKPVVRVNVKGNKSIAPAEGRNRYDGIYK 298
DB 530 LTNMRALALNCDAPLDKIGAESNRNWRAGKPVVIRSPKRIKSIYAEENRYDGIYK 589
QY 299 VKYWPKEGKS-CFLVWRYLLRRDDDEPGPWTEGKDRICKLGLTMOYEGYLEALANRE 357
DB 590 VKYWPESISSHGFLVWRYLLRRDDVEPAPWTSEGIERSRLRLRLQYPAGY-----PSD 644
QY 358 REKENSKEEEQEGGFASPTGKWKWRKSGAGGFSRAGSPRRTSKTKVPEYSLTAQ 417
DB 645 KEGKPKQSKKQPSGTTKRP-----ISDDDCPSASKVYKASDSAEATEAFQLTPQ 695
QY 418 QSSLIREDKSNAKLWNEVLASLKORPASGSPFQLFLSKVETFOICCOELVFRBITTVVC 477
DB 696 QOHLIREDCQKQKLMDEVLHLVEGPN-----FLKKLEQSFMCVCCQELVYQPVTTTC 748
QY 478 QHNVCCKCLDRSFRAQVFCSPACRYDLGRSYAMQVNPQLQTVLNQLFPYGYNGR 531
DB 749 FHNVCCKCLQRSFRAQVFCSPACRHDLCQNTIMPNEILQTLILLDLFFPYGSKGR 802
RESULT 11
ABM83220
ID ABM83220 standard; protein; 770 AA.
XX AC ABM83220;
XX 18-NOV-2004 (first entry)
XX Human diagnostic and therapeutic pprotein SEQ ID NO:3469.
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
XX WO2004023973-A2.
XX 25-MAR-2004.
XX 12-SEP-2003; 2003WO-US028227.
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AW, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX WPI: 2004-329368/30.
XX N-PSDB; ACN41872.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX Claim 27; Page; 190pp; English.
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX Sequence 770 AA;
SQ

Query Match 53.9%; Score 1562; DB 8; Length 770;
Best Local Similarity 54.5%; Pred. No. 2.4e-134;
Matches 291; Conservative 75; Mismatches 112; Indels 56; Gaps 7;

QY 1 DDLNDCKRIIFVDEVFKEIPEGSGPM--VDNPMRKSGPSCKHCKDDVNLRCVACHL 58
DB 290 EGTLDNDCKIISVDEIFKIERPG-AHPLSFADGKFLRRNDPECDLGGDPKCKHCHSCSRV 348
QY 59 CGGRQDPDKQLMCDCEMFAHYICLDPLSSVPSDEWYCPCEKNDASVVLGRLRES 118
DB 349 CGGKEPNQQLDCDCNAYHYICLNPDLKVPBEEYWCPSCKTDSSEVVKAGERLWS 408
QY 119 KKNKMASATSSQORDWKGMAVCGRTECTIVPSNHYGPIPIGVGTWRRFRVQVSSG 178
DB 409 KKKAKMPSASTESRRDWRGMAVCGRTECTIVPSNHYGPIPIGVGTWRRFRVQVSEAG 468
QY 179 VHRPHVAGIHGRSNDGSLVLAGGVDDVDHGNFTYTGSGGRDLGNGKRTAESCDQK 238
DB 469 VHRPHVGGIHGRSNDGAYSLVLAGGFADVDGRDFTYTGSGGKNLGNKRIGAPSADQT 528
QY 239 LTNTRALALNCFAPINDOGEAKDWRSGKPVVRVNVKGGKNSKYAPAEGRNVDGIYK 298
DB 529 LTNMRALALNCDAFLDDDKIGAESNRWAG-----558
QY 299 VVYKWEPEKGS-GFLVWRYLLRRDDDEPGPWTKEGDKRIKGLTLWQVPEGYLEALANRE 357
DB 559 -VKYWEPEISSHGFLVWRYLLRRDDVEPAPWTSEGIERSRRLCLRLQVPAGY-----PSD 612
QY 358 REKENSKEEERQEGGFASPTGKGKWKRKAGGSPSPAGSPRTSKTKVPEYSLTAQ 417
DB 613 KEGKPKGQSKQPSGTTKRP-----ISDDDCPSASKVYKASDSAEALFNQLTQP 663
QY 418 QSLIREDKSNKLNWELASLKORPASGSPQLFLSKVEETFCQICCOELVPRPTTVTC 477
DB 664 QQLHREDQCNQKLWDELVSHLVEGN-----FLKLEQFMVCCQELVQVPTTEC 716
QY 478 QHNVCCKDLDRFRAQVFCSPACRYDLGRSVMQVNPQLQTLVNLQFLGYGNGR 531
DB 717 FHNVCCKDLQRSFKAQVFCSPACRHDLDGQYIMFNEIQLTLDLFFPGYSNGR 770

RESULT 12
ABU69599
ID ABU69599 standard; protein; 645 AA.
XX ABU69599;
XX
XX
DT 05-JUN-2003 (first entry)
XX
DE Human NF-kappaB associated polypeptide sequence #5.
XX
XX Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;
KW inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;
KW haematopoietic tumour; hyper-IgM syndrome; viral infection; asthma;
KW hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV;
KW X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti;
KW influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW experimental allergic encephalomyelitis; autoimmune disorder; wound;
KW hyper immune activity; acute phase response; hypercongenital condition;
KW birth defect; necrotic lesion; organ transplant rejection; pancreas;
KW signal transduction; hyperproliferative disorder; diabetes mellitus;
KW vitamin B12 malabsorption; neurological disorder; Huntington's chorea;
KW Turner's syndrome; bacterial infection; cardiovascular disorder;
KW infertility; psoriasis; haemolytic anaemia; antiinflammatory; anti-HIV;
KW cytostatic; hepatotropic; virucide; antirheumatic; antiarthritic;
KW antiasthmatic; immunomodulator; antidiabetic; antiallergic;
KW neuroprotective; immunosuppressive; vulnerary; antibacterial;
KW antiinfertility; antianaeamic; antipsoriatic; cerebroprotective; cardiant;
KW antiarteriosclerotic.
XX
XX Homo sapiens.
OS

XX WO200286076-A2.
XX 31-OCT-2002.
XX
XX 19-APR-2002; 2002WO-US012636.
XX
XX 19-APR-2001; 2001US-0284962P.
PR 26-APR-2001; 2001US-0286645P.
PR 09-JAN-2002; 2002US-0346986P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Carman J, Feder J, Nadler S;
XX WPI; 2003-093119/08.
DR N-PSDB; ACA54638.
XX
XX Novel NF-kappaB-associated polypeptides and polynucleotides useful for
PT diagnosing, treating and preventing cancer, hepatic disorders, aberrant
PT apoptosis, viral infections, autoimmune disorders, asthma and stroke.
XX
XX Claim 6; Page 493-494; 608pp; English.
XX
XX The present invention relates to the isolation of human nuclear factor-
CC kappaB (NF-kappaB) associated polypeptides and polynucleotides. The NF-
CC kappaB associated polypeptide and polynucleotide sequences are useful for
CC preventing, treating or ameliorating various disorders including immune
CC disorders, inflammatory disorders, cancers, disorders relating to
CC aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,
CC haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal
CC dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al
CC incontinentia pigmenti, viral infections (e.g. those caused by human
CC immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),
CC hepatitis B, hepatitis C, Epstein Barr virus (EBV), influenza),
CC rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,
CC atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental
CC allergic encephalomyelitis (EAE), autoimmune disorders, disorders related
CC to hyper immune activity, disorders related to aberrant acute phase
CC responses, hypercongenital conditions, birth defects, necrotic lesions,
CC wounds, organ transplant rejection, disorders related to aberrant signal
CC transduction, hyperproliferative disorders, diseases of the pancreas
CC (e.g. diabetes mellitus, vitamin B12 malabsorption), neurological
CC disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial
CC infections, cardiovascular disorders, infertility, psoriasis and
CC haemolytic anaemia. The present sequence represents a human NF-kappaB
CC associated polypeptide of the invention
XX
XX Sequence 645 AA;
QY
Query Match 44.8%; Score 1297; DB 6; Length 645;
Best Local Similarity 67.2%; Pred. No. 5.1e-110;
Matches 231; Conservative 48; Mismatches 61; Indels 4; Gaps 3;

QY 1 DDLNDCKRIIFVDEVFKEIPEGSGPM--VDNPMRKSGPSCKHCKDDVNLRCVACHL 58
DB 291 EGTLDNDCKIISVDEIFKIERPG-AHPLSFADGKFLRRNDPECDLGGDPKCKHCHSCSRV 349
QY 59 CGGRQDPDKQLMCDCEMFAHYICLDPLSSVPSDEWYCPCEKNDASVVLGRLRES 118
DB 350 CGGKEPNQQLDCDCNAYHYICLNPDLKVPBEEYWCPSCKTDSSEVVKAGERLWS 409
QY 119 KKNKMASATSSQORDWKGMAVCGRTECTIVPSNHYGPIPIGVGTWRRFRVQVSSG 178
DB 410 KKKAKMPSASTESRRDWRGMAVCGRTECTIVPSNHYGPIPIGVGTWRRFRVQVSEAG 469
QY 179 VHRPHVAGIHGRSNDGSLVLAGGVDDVDHGNFTYTGSGGRDLGNGKRTAESCDQK 238
DB 470 VHRPHVGGIHGRSNDGAYSLVLAGGFADVDGRDFTYTGSGGKNLGNKRIGAPSADQT 529
QY 239 LTNTRALALNCFAPINDOGEAKDWRSGKPVVRVNVKGGKNSKYAPAEGRNVDGIYK 298
DB 530 LTNMRALALNCDAFLDDDKIGAESNRWAGKPVVRVIRSPFKGRKISKYAPEGRNVDGIYK 589

QY 299 VVKYWEKGS-GFLVWRYLLRRDDDEPGPWTKEGKDKRIKKLGL 341
 Db 590 VVKYWEISSHGHFLVWRYLLRRDDVEPAPWTSEGIERSRLCL 633
 RESULT 13
 ABU69620
 ID ABUS9620 standard; protein; 645 AA.
 XX AC ABU69620;
 DT 05-JUN-2003 (first entry)
 XX Human NF-kappaB associated polypeptide sequence #23.
 DE Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;
 XX inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;
 KW haematopoietic tumour; hyper-IgM syndrome; viral infection; asthma;
 KW hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV;
 KW X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti;
 KW influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW experimental allergic encephalomyelitis; autoimmune disorder; wound;
 KW hyper immune activity; acute phase response; hypercongenital condition;
 KW birth defect; necrotic lesion; organ transplant rejection; pancreas;
 KW signal transduction; hyperproliferative disorder; diabetes mellitus;
 KW vitamin B12 malabsorption; neurological disorder; Huntington's chorea;
 KW Turner's syndrome; bacterial infection; cardiovascular disorder;
 KW infertility; psoriasis; haemolytic anaemia; antiinflammatory; anti-HIV;
 KW cytostatic; hepatotropic; virucide; antirheumatic; antiarthritic;
 KW antiasthmatic; immunomodulator; antidiabetic; antiallergic;
 KW neuroprotective; immunosuppressive; vulnerary; antibacterial;
 KW antifertility; antianaemic; antipsoriatic; cerebroprotective; cardiant;
 KW antiarteriosclerotic.
 XX Homo sapiens.
 XX WO200286076-A2.
 XX 31-OCT-2002.
 XX 19-APR-2002; 2002WO-US012636.
 XX 19-APR-2001; 2001US-0284962P.
 PR 26-APR-2001; 2001US-0286645P.
 PR 09-JAN-2002; 2002US-0346986P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA Carman J, Feder J, Nadler S;
 PI WPI; 2003-093119/08.
 DR N-PSDB; ACA54638.
 XX Novel NF-kappaB-associated polypeptides and polynucleotides useful for
 PT diagnosing, treating and preventing cancer, hepatic disorders, aberrant
 PT apoptosis, viral infections, autoimmune disorders, asthma and stroke.
 XX Claim 4; Page 497-499; 608pp; English.
 PS The present invention relates to the isolation of human nuclear factor-
 CC kappaB (NF-kappaB) associated polypeptides and polynucleotides. The NF-
 CC kappaB associated polypeptide and polynucleotide sequences are useful for
 CC preventing, treating or ameliorating various disorders including immune
 CC disorders, inflammatory disorders, cancers, disorders relating to
 CC aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,
 CC haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal
 CC dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al
 CC incontinentia pigmenti, viral infections (e.g. those caused by human
 CC immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),
 CC hepatitis B, hepatitis C, Epstein Barr virus (EBV), influenza),
 CC rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,

CC atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental
 CC allergic encephalomyelitis (EAE), autoimmune disorders, disorders related
 CC to hyper immune activity, disorders related to aberrant acute phase
 CC responses, hypercongenital conditions, birth defects, necrotic lesions,
 CC wounds, organ transplant rejection, disorders related to aberrant signal
 CC transduction, hyperproliferative disorders, diseases of the pancreas
 CC (e.g. diabetes mellitus, vitamin B12 malabsorption), neurological
 CC disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial
 CC infections, cardiovascular disorders, infertility, psoriasis and
 CC haemolytic anaemia. The present sequence represents a human NF-kappaB
 CC associated polypeptide of the invention
 XX SQ Sequence 645 AA;
 Query Match 44.8%; Score 1297; DB 6; Length 645;
 Best Local Similarity 67.2%; Pred. No. 5.1e-110;
 Matches 231; Conservative 48; Mismatches 61; Indels 4; Gaps 3;
 QY 1 DDSLNDCHRIIFVDEVKIERPGEQSPM--VDPNMRKSGSPCKHCKDDVNRLLCRVCACHL 58
 Db 291 EGTLNDCKLIISVDIFKIEREG-AHPLSFADGKFLRRNDPCDLCGGDPKCKHSCSCR 349
 QY 59 CGGRQDDPKQLMCDCECMAPHYICLDPPPLSSVPSSEDEWYCPCECRNDASEVVLAGERLRES 118
 Db 350 CGGRHEPNWQLLDCENVAHYICLNPLDKVPBEEYWCPSCKTDSSEVVKAGERLKMS 409
 QY 119 KKNAMASATSSORDWKGWACVGRTECTIVPSNHYGPIPIGVGTWFRVQVSSSG 178
 Db 410 KKAAMPASSTESRRDWRGMACVGRTECTIVPSNHYGPIPIGVGTWFRVQVSSAG 469
 QY 179 VHRPHVAGHGRSNDGYSVLVAGYEDVDVHGPFYTGSGGRDLGKRTAEQSCDQK 238
 Db 470 VHRPHVAGHGRSNDGYSVLVAGYEDVDVHGPFYTGSGGRDLGKRTAEQSCDQK 529
 QY 239 LTNTNRALALNCFAPINDQGAEGAKDWRSGKPVVRVNVKGGKNSKYAPAEGRNYDGIYK 298
 Db 530 LTNNRALLNCDAPLDDKIGAESRNRWAGKPVVRVIRSKRTISKYAPAEGRNYDGIYK 589
 QY 299 VVKYWEKGS-GFLVWRYLLRRDDDEPGPWTKEGKDKRIKKLGL 341
 Db 590 VVKYWEISSHGHFLVWRYLLRRDDVEPAPWTSEGIERSRLCL 633
 RESULT 14
 ABB76983
 ID ABB76983 standard; protein; 174 AA.
 XX AC ABB76983;
 DT 22-JUL-2002 (first entry)
 XX Human Inverted CCAAT box binding protein, ICBP90, fragment #3.
 DE Human; inverted CCAAT box binding protein; ICBP90; cytostatic;
 KW cell proliferation control; inverted CCAAT box; cancer.
 XX Homo sapiens.
 XX WO200078949-A1.
 XX 28-DEC-2000.
 XX 22-JUN-2000; 2000WO-FR001747.
 XX 22-JUN-1999; 99FR-00007935.
 PA (ADSR-) ADEREGEM ASSOC DEV RECH EN GENETIQ.
 PI Bronner C, Hopfner R, Mousli M, Jeltsch J, Lutz Y, Oudet P;
 XX WPI; 2001-091571/10.
 DR N-PSDB; ABL58023.
 XX

PT Novel inverted CCAAT box binding protein, and related nucleic acids,
PT antibodies and specific ligands, useful for treating and preventing
PT cancer.
XX
PS Claim 2; Page 103; 115pp; French.
XX
CC The present sequence is a protein fragment of human ICBP90 (inverted
CC CCAAT box binding protein). The inverted CCAAT box is implicated in cell
CC proliferation control. Several copies of the inverted CCAAT box are
CC present in the promoter of the topoisomerase IIalpha gene, and also
CC functions as a nuclear receptor. ICBP90 (AB076980) and its coding
CC sequence (AB08020) are useful for treatment and/or prevention of cancer
XX
SQ Sequence 174 AA;
Query Match 32.0%; Score 926; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 358 REKENSKEEERQEGGFASPRTGKWKVKRSAGGSPRAGSPRRTSKTKVPEYSLTAQ 417
DB 1 REKENSKEEERQEGGFASPRTGKWKVKRSAGGSPRAGSPRRTSKTKVPEYSLTAQ 60
QY 418 QSLREDKSNKLNWNEVLASLKDRLPASGSPFLFLSKVEETFCICCOELVFRPITTV 477
DB 61 QSLREDKSNKLNWNEVLASLKDRLPASGSPFLFLSKVEETFCICCOELVFRPITTV 120
QY 478 QHNVCCKDLDRSFRAQVFSCPCRYDLGRSYAMQVNPQLOTVLNQLFPGYGNR 531
DB 121 QHNVCCKDLDRSFRAQVFSCPCRYDLGRSYAMQVNPQLOTVLNQLFPGYGNR 174
RESULT 15
ABP64013
ID ABP64013 standard; protein; 198 AA.
XX
AC ABP64013;
XX
DT 04-NOV-2002 (first entry)
XX
DE Human ORF393.
XX
KW Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnary;
KW Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet;
KW human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;
KW cancer; cardiovascular disease; allergy; autoimmune disease;
KW wound healing; blood coagulation disorder; inflammatory disorder.
XX
OS Homo sapiens.
XX
PN US2002082206-A1.
XX
PD 27-JUN-2002.
XX
PF 30-MAY-2001; 2001US-00867550.
XX
PR 30-MAY-2000; 2000US-0208427P.
XX
PA (LEAC/) LEACH M D.
PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.
XX
PI Leach MD, Mehraban F, Conley PB, Topper JN, Law D;
XX
DR WPI; 2002-626554/67.
DR N-PSDB; ABQ98576.
XX
PT New polypeptide designated ORFX are present in human atherogenic cells
PT and are useful to prevent and treat ORFX-associated disorders including
PT cancer, allergy, wound healing or autoimmune, cardiovascular or
PT inflammatory disease.

XX Claim 10; SEQ ID NO 766; 78pp; English.
PS
XX
CC The present invention relates to novel human ORFX polypeptides and their
CC coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences
CC were discovered in human atherogenic cells, in particular in platelets
CC and human umbilical vein endothelial cells (HUVEC) and are expressed in
CC many other tissues as well. Atherogenic cells are cells which have the
CC potential to develop atherosclerotic plaques. The ORFX polypeptides and
CC nucleic acids are useful for treating or preventing a pathological
CC condition associated with an ORFX-associated disorder, e.g. cancer,
CC cardiovascular disease, allergy, autoimmune disease, wound healing, blood
CC coagulation disorders or inflammatory disorders. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/sequence.html?DocID=20020082206
XX
SQ Sequence 198 AA;
Query Match 28.4%; Score 823.5; DB 5; Length 198;
Best Local Similarity 75.8%; Pred. No. 4e-67;
Matches 150; Conservative 22; Mismatches 25; Indels 1; Gaps 1;
QY 122 AKMASATSSQORDWCKGMACVGRTECTIVPSNHYGPIPGIPVGTWFRVQVSSGVHR 181
DB 1 AKMPSASTESRRDWGRGMACVGRTECTIVPSNHYGPIPGIPVGTWFRVQVSSGVHR 60
QY 182 PHVAGIHGRSNDGYSYSLVLAGGYEDVDHGNFFVTYTGSGRDLSCNKRRTAESCDQKLTN 241
DB 61 PHVGGIHGRSNDGAYSLSVLAGGFADVDGRDEFTYTGSGGKNLGNKKGAPSAQDTLTN 120
QY 242 TNRALALNCFAPINDQEGAEAKDWRSGKPVRRVNRVKGKNSKYAPAEGRNRYDGIYKVVK 301
DB 121 MNRALALNCDAPLDDDKIGAESRNRWAGKPVRRVIRSFKGRKISKYAPAEGRNRYDGIYKVVK 180
QY 302 YWPEKGKS-GFLVWRYLL 318
DB 181 YWPEISSSHGFLVWRYLL 198
Search completed: July 25, 2005, 17:03:40
Job time : 170 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 25, 2005, 16:39:26 ; Search time 179 Seconds
(without alignments)
1519.073 Million cell updates/sec

Title: US-10-019-071-2_COPY_263_793
Perfect score: 2896
Sequence: 1 DDSLNDLCRIIFVDFVKIER.....VNQPLQTLVNLQFFGYNGR 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2896	100.0	793	Q9P115	Q9p115 homo sapien
2	2887	99.7	793	Q9T88	Q9t88 homo sapien
3	2212	76.4	829	Q7TPK1	Q7tpk1 rattus norv
4	2169	74.9	782	Q8YDF2	Q8ydf2 mus musculus
5	2165	74.8	782	Q9Z1H6	Q9z1h6 mus musculus
6	2069.5	71.5	775	Q6PEI0	Q6pei0 brachydanio
7	2062	71.2	776	Q6DRP6	Q6drp6 brachydanio
8	1758.5	60.7	803	Q7TMI3	Q7tmi3 mus musculus
9	1757.5	60.7	803	Q8KLI5	Q8kli5 mus musculus
10	1718.5	59.3	802	Q96PU4	Q96pu4 homo sapien
11	1544	53.3	597	Q6IP39	Q6ip39 xenopus lae
12	1207	41.7	299	Q8C6F1	Q8c6f1 mus musculus
13	1005	34.7	189	Q9H6S6	Q9h6s6 homo sapien
14	886	30.6	474	Q8VIA1	Q8via1 mus musculus
15	816.5	28.2	516	Q8BJP6	Q8bjp6 mus musculus
16	792.5	27.4	503	Q8TAG7	Q8tag7 homo sapien
17	732	25.3	139	Q8J022	Q8j022 homo sapien
18	688	21.0	645	Q8VYZ0	Q8vyz0 arabidopsis
19	600	20.7	641	Q9FV83	Q9fv83 arabidopsis
20	591.5	20.4	617	Q67XP0	Q67xp0 arabidopsis
21	588.5	20.3	617	Q9FKA7	Q9fka7 arabidopsis
22	560	19.3	615	Q6NQ90	Q6nc90 arabidopsis
23	556	19.2	622	Q9C8E1	Q9c8e1 arabidopsis
24	556	19.2	623	Q680I0	Q68i0 arabidopsis
25	553.5	19.1	765	Q7XW58	Q7xw58 oryza sativ
26	533.5	18.4	598	Q9C8E0	Q9c8e0 arabidopsis
27	524	18.1	789	Q7SM36	Q7sm36 oryza sativ
28	514.5	17.8	610	Q9FW25	Q9fw25 oryza sativ
29	473	16.3	650	Q9FV82	Q9fv82 arabidopsis
30	427	14.7	461	Q8I463	Q8i463 arabidopsis
31	424	14.6	465	Q681I0	Q681i0 arabidopsis

32 420.5 14.5 167 2 Q659C8 Q659c8 homo sapien
33 353.5 12.2 432 2 O22280 O22280 arabidopsis
34 335 11.6 434 2 Q8H9A3 Q8h9a3 arabis genm
35 311.5 10.8 299 2 Q9RU61 Q9ru61 deinococcus
36 310.5 10.7 301 2 Q9ADDA Q9add4 streptomyce
37 279 9.6 684 2 Q7XHM7 Q7xhm7 oryza sativ
38 270.5 9.3 794 1 SUV5_ARATH SUV5_arath arabidopsis
39 263 9.1 48 2 Q9P1U7 Q9p1u7 homo sapien
40 263 9.1 790 1 SUV6_ARATH SUV6_arath arabidopsis
41 252.5 8.7 624 1 SUV4_ARATH SUV4_arath arabidopsis
42 248.5 8.6 766 2 Q8H6E0 Q8h6e0 zea mays (m
43 247.5 8.5 921 2 Q6K4E6 Q6k4e6 oryza sativ
44 237.5 8.2 908 2 Q6ZJS9 Q6zjs9 oryza sativ
45 235.5 8.1 670 1 SUV1_ARATH SUV1_arath arabidopsis

ALIGNMENTS

RESULT 1
Q9P115 PRELIMINARY; PRT; 793 AA.
AC Q9P115;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transcription factor ICBP90.
GN Name=ICBP90;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20110783; PubMed=10646863;
RA Hopfner R., Mouli M., Jeltsch J.M., Voulgaris A., Lutz Y., Marin C.,
RA Bellocq J.P., Oudet P., Bronner C.;
RT "ICBP90, a novel human CCAAT binding protein, involved in the
RT regulation of topoisomerase I α expression.";
RL Cancer Res. 60:121-128(2000).
DR EMBL; AF129507; AAF28469.1; -.
DR HSSP; Q9UIG0; 1F62.
DR GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; TAS.
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; TAS.
DR InterPro; IPR011011; FYVE_PHD_Znf.
DR InterPro; IPR003105; SRA_YDG.
DR InterPro; IPR000626; Ubiquitin.
DR InterPro; IPR001965; Znf_PHD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR PRINTS; PR00348; UBIQUITIN.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00184; RING; 2.
DR SMART; SM00466; SRA; 1.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS50016; ZF_PHD_2; 1.
DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
DR PROSITE; PS50089; ZF_RING_2; 2.
SQ SEQUENCE 793 AA; 89815 MW; D9B4161E892BB014 CRC64;

Query Match 100.0%; Score 2896; DB 2; Length 793;
Best Local Similarity 100.0%; Pred. No. 5.5e-191;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DDSLNDLCRIIFVDFVKIERPGESPMVDNPMRRKSGPSCKHCKDDVNRLCRVACHLCG 60
DB 263 DDSLNDLCRIIFVDFVKIERPGESPMVDNPMRRKSGPSCKHCKDDVNRLCRVACHLCG 322

```
QY 61 GQDDPKQLMCDCECMAPHIYCLDPLSSVPSEDEWYCPCERNDADEVVLAGERLRESKK 120
Db 323 GQDDPKQLMCDCECMAPHIYCLDPLSSVPSEDEWYCPCERNDADEVVLAGERLRESKK 382
QY 121 NAKMASATSSORDMGKMACVGRKTECTIVPSNHYGPIPGIPVGTMMRFVQVSESGVH 180
Db 383 NAKMASATSSORDMGKMACVGRKTECTIVPSNHYGPIPGIPVGTMMRFVQVSESGVH 442
QY 181 RPHVAGIHGRSNDGYSYLVLAGYEDDDVHGNFFYTTGSGGRDLGSKNRTAQSQCOKLIT 240
Db 443 RPHVAGIHGRSNDGYSYLVLAGYEDDDVHGNFFYTTGSGGRDLGSKNRTAQSQCOKLIT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNRYDGIYKV 300
Db 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNRYDGIYKV 562
QY 301 KYWPEKSGSGLVWRYLLRRDDDEPGPWTKEGDKRIKKLGLTMQYPEGYLEALANREREK 360
Db 563 KYWPEKSGSGLVWRYLLRRDDDEPGPWTKEGDKRIKKLGLTMQYPEGYLEALANREREK 622
QY 361 ENSKREEBEQGGFASPRGTGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 420
Db 623 ENSKREEBEQGGFASPRGTGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 682
QY 421 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFQCICQELVFRPITTVCOHN 480
Db 683 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFQCICQELVFRPITTVCOHN 742
QY 481 VCKDCLDRSFRAQVFCSPACRYDLGRSYAMQVNPLOTVLNQLFPYGNR 531
Db 743 VCKDCLDRSFRAQVFCSPACRYDLGRSYAMQVNPLOTVLNQLFPYGNR 793

RESULT 2
Q96T88 PRELIMINARY; PRT; 793 AA.
AC Q96T88;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Nucleic acid zinc finger protein Np95.
GN Name=UHRF1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Davenport J.W., Fernandes E.R., Neale G.A.M., Goorha R.M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF274048; AAKS5744.1; -.
DR HSSP; Q9UIG0; 1F62.
DR Genew; HGNC:12556; UHRF1.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR011011; FYVE PHD_Znf.
DR InterPro; IPR003105; SRA_YDG_Znf.
DR InterPro; IPR000626; Ubiquitin.
DR InterPro; IPR001965; Znf PHD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR PRINTS; PF02182; YDG_SRA; 1.
DR PRINTS; PF00348; UBIQUITIN.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00184; RING; 2.
DR SMART; SM00466; SRA; 1.
DR SMART; SM00213; UBQ; 1.
```

```
DR PROSITE; PS0053; UBIQUITIN 2; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
DR PROSITE; PS00089; ZF_RING_2; 2.
SQ SEQUENCE 793 AA; 89813 MW; E65B15657525C89F CRC64;

Query Match 99.7%; Score 2887; DB 2; Length 793;
Best Local Similarity 99.6%; Pred. No. 2.3e-190;
Matches 529; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDLSNDCRIIFVDEVFKIERPEGSPMVDNPMRRKSGPSCKHCKDDVNRLCRVCACHLCG 60
Db 263 DDLSNDCRIIFVDEVFKIERPEGSPMVDNPMRRKSGPSCKHCKDDVNRLCRVCACHLCG 322
QY 61 GRQDDPKQLMCDCECMAPHIYCLDPLSSVPSEDEWYCPCERNDADEVVLAGERLRESKK 120
Db 323 GRQDDPKQLMCDCECMAPHIYCLDPLSSVPSEDEWYCPCERNDADEVVLAGERLRESKK 382
QY 121 NAKMASATSSORDMGKMACVGRKTECTIVPSNHYGPIPGIPVGTMMRFVQVSESGVH 180
Db 383 NAKMASATSSORDMGKMACVGRKTECTIVPSNHYGPIPGIPVGTMMRFVQVSESGVH 442
QY 181 RPHVAGIHGRSNDGYSYLVLAGYEDDDVHGNFFYTTGSGGRDLGSKNRTAQSQCOKLIT 240
Db 443 RPHVAGIHGRSNDGYSYLVLAGYEDDDVHGNFFYTTGSGGRDLGSKNRTAQSQCOKLIT 502
QY 241 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNRYDGIYKV 300
Db 503 NTNRLALNCFAPINDQEGAEAKDWRSGKPVVRVNRVKGKNSKYAPAEGRNRYDGIYKV 562
QY 301 KYWPEKSGSGLVWRYLLRRDDDEPGPWTKEGDKRIKKLGLTMQYPEGYLEALANREREK 360
Db 563 KYWPEKSGSGLVWRYLLRRDDDEPGPWTKEGDKRIKKLGLTMQYPEGYLEALANREREK 622
QY 361 ENSKREEBEQGGFASPRGTGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 420
Db 623 ENSKREEBEQGGFASPRGTGKWKRSAGGSPRAGSPRRTSKTKVPEYSLTAQOSS 682
QY 421 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFQCICQELVFRPITTVCOHN 480
Db 683 LIREDKSNAKLWNEVLASLKDPRASGSPFQLFLSKVEETFQCICQELVFRPITTVCOHN 742
QY 481 VCKDCLDRSFRAQVFCSPACRYDLGRSYAMQVNPLOTVLNQLFPYGNR 531
Db 743 VCKDCLDRSFRAQVFCSPACRYDLGRSYAMQVNPLOTVLNQLFPYGNR 793

RESULT 3
Q7TPK1 PRELIMINARY; PRT; 829 AA.
AC Q7TPK1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AC2-121.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu C.S., Li W.Q., Li Y.C., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J.,
RA Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F., Han H.P.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY321334; AAP86266.1; -.
DR HSSP; Q9UIG0; 1F62.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
```



```
DR GO: 0006355; P: regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR011011; FYVE_PHD_Znf.
DR InterPro: IPR002345; Lipocalin.
DR InterPro: IPR003105; SRA_YDG.
DR InterPro: IPR000626; Ubiquitin.
DR InterPro: IPR001965; Znf_PHD.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00628; PHD; 1.
DR Pfam: PF00240; ubiquitin; 1.
DR Pfam: PF02182; YDG_SRA; 1.
DR SMART: SM00249; PHD; 1.
DR SMART: SM00184; RING; 2.
DR SMART: SM00466; SRA; 1.
DR SMART: SM00213; UBQ; 1.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE: PS00053; UBIQUITIN_2; 1.
DR PROSITE: PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE: PS00016; ZF_PHD_2; 1.
DR PROSITE: PS00518; ZF_RING_1; UNKNOWN_1.
DR PROSITE: PS00089; ZF_RING_2; 1.
SQ SEQUENCE 829 AA; 93222 MW; E688327F33FE74BE CRC64;

Query Match 76.4%; Score 2212; DB 2; Length 829;
Best Local Similarity 75.9%; Pred. No. 7.6e-144; Indels 18; Gaps 7;
Matches 404; Conservative 58; Mismatches 52;

QY 1 DDLNDLCRIIFVDEVFKEIERGEGSPMVDNPMRRKSGPSCKRCKDDVNRCLRCVACHLCG 60
DB 315 DSQLNNCRIIFVDEVILKIELPNERPLIGSPSRKSGPSCQYCKDDENKPCRKCACHICG 374

QY 61 GRQDPDKQLMCDCEMAFHICYCLDPLSSVPEDEWYCEPCNRDASEVVLAGEIRRESKK 120
DB 375 GREAPEKQVLCDECDMAFHLYCLQPLTCTVPEPEWYCPSCRTDSSEVVQAGEKLKSKK 434

QY 121 NAKMASATSSORDKMGKMACVGRTECTIVPSNHYGPIPGIPVGTMTWFRVQVSESGVH 180
DB 435 KAKMASATSSRRDDMGKMACVGRTECTIVPANHPGPIPGVPGVTMTWFRVQVSESGVH 494

QY 181 RPHVAGIHRSGDSYSLVLAGYEDVDHGNFFVTYSGGRDLGSGNKRKTAEQSDQKLT 240
DB 495 RPHVAGIHRSGNDGYSYLVLAGYEDVDHGNFFVTYSGGRDLGSGNKRKTAEQSDQKLT 554

QY 241 NTRALALNCFAPINDQGAEKAKWRSGKPVVRVNRVVGKGNKSYAPAEGRNYDGIYKV 300
DB 555 NNRALALNCHSPIN-EKGAEAEDWRQKPVVRVNRVNRMGKSKYAPAEGRNYDGIYKV 613

QY 301 KYWPEKSGKGLVWRYLLRRDDDEPCWTKGDKRIKGLITWQYPEGVLEALANRERK 360
DB 614 KYWPEKSGKGLVWRYLLRRDDDEPEPTWREGKDRTRQLGLTMQYPEGVLEALANKEK-- 671

QY 361 ENSKREBEQOEGFPASPTGK-GKWKRKSAGGSPSRAGSPRRTSKTKVPEYSLTAQOS 419
DB 672 -NRKRPKALEOG----PSSKIGKSKRSTGPATT----SP-RVSKSKLEPYTLPLQQA 722

QY 420 SLIREDKSNALWNEVLAISKDRPASGSPFLQSLKVEETFOCICQELVFPRTTVCQH 479
DB 723 NLIKEDKGNKALWDDVLSLQD-----GPIQIFLSKVKEAFQCICQELVFPRTTVCQH 777

QY 480 NVCKDCLDRSFRQAQVSCACRYDLGRSYAMQVNPLOTVLNQLPFGYNGR 531
DB 778 NVCKDCLDRSFRQAQVSCACRYDLDRHSSPFRVNPLOTVLNQLPFGYNGR 829

RESULT 4
Q8VDF2 PRELIMINARY; PRT; 782 AA.
AC Q8VDF2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ubiquitin-like, containing PHD and RING finger domains, 1.
GN Name=Uhrf1;
OS Mus musculus (Mouse).
```

```
OC GO: 0006355; P: regulation of transcription, DNA-dependent; IEA.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CZSCH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CZSCH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022167; AAH22167.1; -.
DR HSP; O9UIG0; 1P62.
DR MGD; MGI:1338889; Uhrf1.
DR GO: 0005634; C:nucleus; TAS.
DR GO: 0000828; P:cell proliferation; TAS.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR PRINTS; PR00348; UBIQUITIN.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00184; RING; 2.
DR SMART; SM00466; SRA; 1.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE; PS00053; UBIQUITIN_2; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
DR PROSITE; PS00089; ZF_RING_2; 2.
SQ SEQUENCE 782 AA; 88319 MW; DC5EEDFCDF779074 CRC64;

Query Match 74.9%; Score 2169; DB 2; Length 782;
Best Local Similarity 74.0%; Pred. No. 6.5e-141;
Matches 399; Conservative 58; Mismatches 55; Indels 24; Gaps 7;

QY 1 DDLNDLCRIIFVDEVFKEIERGEGSPMVDNPMR-----RKSGPSCKKCKDDVNRCLCR 52
DB 260 DSQLNNCRIIFVDEVILPNERPLIASQPPPALNTGKSGPSCKRCKDDENKPCR 319

QY 53 VCACHLCGGRQDPDKQLMCDCEMAFHICYCLDPLSSVPEDEWYCEPCNRDASEVVLG 112
DB 320 KCACHVCGGRAPEKQLLCDECDMAFHLYCLKPLTSTVPEPEWYCPSCRTDSSEVVQAG 379

QY 113 ERLRESKKNKAKMASATSSSQDRDWGKMACVGRTECTIVPSNHYGPIPGIPVGTMTWFRV 172
DB 380 EKLKESKKKAKMASATSSRRDRDWGKMACVGRTECTIVPANHPGPIPGVPGVTMTWFRV 439

QY 173 QVSESGVHRPHVAGIHRSGDSYSLVLAGYEDVDHGNFFVTYSGGRDLGSGNKRKTAE 232
DB 440 QVSESGVHRPHVAGIHRSGDSYSLVLAGYEDVDHGNFFVTYSGGRDLGSGNKRKTAE 499
```

```
QY 233 QSCDQKLTNNRRLALNCFAPINDOEGAEAKDWRSGKPVVRVNVKGGKNSKYAPAEGR 292
DB 500 QSDQKLTNNRRLALNCHSPIN-EKGAEADWRGKPVVRVNVKGGKSHKYAPAEGR 558
QY 293 YDGIYKVKYWPKEGKSGFLVWRYLLRRDDDPGWTKEGDKRIKKLGLTMOYPEGYLEA 352
DB 559 YDGIYKVKYWPKEGKSGFLVWRYLLRRDDTEPEPWTRGKDRTRQLGLTMOYPEGYLEA 618
QY 353 LANREREKNSKREBEEOEGFASPTGKWKKRSAGGSPRAGSPRTSKTKVBPY 412
DB 619 LAN-----KEKSRKRPAPAKALEQSPSSSKTKGSKQK----STGPT-LSSP-RASKSKSLPEY 668
QY 413 SITAQSSLIREDKSNALNWEVLASLKDPRASGSPFQLFLSKVRETFCICCOELVERP 472
DB 669 TLSEQQANLIKEDKGNALWDDVLTSLQD-----GPYQIFLSKVKEAFQCICCOELVERP 723
QY 473 ITTVQHNVCCKDCLDRSPRAQVFCPCACRYDILGRSYAMQVNOPLQTLNQLPPGYGNGR 531
DB 724 VTTVCQHNVCCKDCLDRSPRAQVFCPCACRYDILGRSYAMQVNOPLQTLNQLPPGYGNGR 782

RESULT 5
Q9Z1H6 PRELIMINARY; PRT; 782 AA.
AC Q9Z1H6
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nuclear protein np95 (Nuclear zinc finger protein Np95).
GN Name=Uhrfl; Synonym=Np95;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pre-Tcell;
RX MEDLINE=99099250; PubMed=9880673;
RA Fujimori A., Matsuda Y., Takemoto Y., Hashimoto Y., Kubo E., Araki R.,
RA Fukumura R., Mita K., Tatsumi K., Muto M.;
RT "Cloning and mapping of Np95 gene which encodes a novel nuclear
RT protein associated with cell proliferation.";
RL Mamm. Genome 9:1032-1035 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Davenport J.W., Fernandes E.R., Neale G.A.M., Goorha R.M.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; D87908; BAA74579.1; -.
DR EMBL; AF274046; AAK55743.1; -.
DR HSSP; Q9UIG0; 1F62.
DR MGD; MGI:1338889; Uhrfl.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR011011; FYVE PHD Znf.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR003105; SRA YDG.
DR InterPro; IPR000626; Ubiquitin.
DR InterPro; IPR001965; Znf PHD.
DR InterPro; IPR001841; Znf PHD.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR Pfam; PF02182; YDG SRA; 1.
DR PRINTS; PR00348; UBIQUITIN.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00184; RING; 2.
DR SMART; SM00466; SRA; 1.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE; PS00553; UBIQUITIN_2; 1.
DR PROSITE; PS01359; ZF PHD 1; UNKNOWN_1.
DR PROSITE; PS00016; ZF PHD 2; 1.
DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
```

```
DR PROSITE; PS50089; ZF_RING_2; 2.
KW Nuclear protein.
SQ SEQUENCE 782 AA; 88303 MW; DC5BEDFCDF69619B CRC64;

Query Match
Best Local Similarity 73.8%; Pred. No. 1.2e-140;
Matches 398; Conservative 59; Mismatches 58; Indels 24; Gaps 7;

QY 1 DDSLNDCKRIIFVDEVKTIERPGEPSPMVDNPMR-----RKSGPSCHKCKDDVNRLCR 52
DB 260 DSQLNNCRIMFVDEVLMIETELPKERRPLIASPPPPALRNTGKSGPSRCFKDDENKPCR 319
QY 53 VCACHLCGRQDPKQMLCDMAFHLYCLDPLLSVPSSEDEWYCPCRDNDASEVLG 112
DB 330 KCACHVCGREAPEKQLLCDMAFHLYCLPLTSVPPPEWYCPCRTDSESVWQAG 379
QY 113 ERLRESKNAKMASATSSQRDWDGKMACVGRTECTIVPSNHYGPIPGIPVGTWWRFRV 172
DB 380 EKLKESKKAKMASATSSRRDWDGKMACVGRTECTIVPANHFQPIFGVPVGTWWRFRV 439
QY 173 QVSSSGVHRPHVAGIHGRSNDGSLVLAGYEDVDVHGNFTYTGSGGRDLSGNKRTAE 232
DB 440 QVSSSGVHRPHVAGIHGRSNDGSLVLAGYEDVDVHGNFTYTGSGGRDLSGNKRTAG 499
QY 233 QSCDQKLTNNRRLALNCFAPINDOEGAEAKDWRSGKPVVRVNVKGGKNSKYAPAEGR 292
DB 500 QSDQKLTNNRRLALNCHSPIN-EKGAEADWRGKPVVRVNVKGGKSHKYAPAEGR 558
QY 293 YDGIYKVKYWPKEGKSGFLVWRYLLRRDDDPGWTKEGDKRIKKLGLTMOYPEGYLEA 352
DB 559 YDGIYKVKYWPKEGKSGFLVWRYLLRRDDTEPEPWTRGKDRTRQLGLTMOYPEGYLEA 618
QY 353 LANREREKNSKREBEEOEGFASPTGKWKKRSAGGSPRAGSPRTSKTKVBPY 412
DB 619 LAN-----KEKSRKRPAPAKALEQSPSSSKTKGSKQK----STGPT-LSSP-RASKSKSLPEY 668
QY 413 SITAQSSLIREDKSNALNWEVLASLKDPRASGSPFQLFLSKVRETFCICCOELVERP 472
DB 669 TLSEQQANLIKEDKGNALWDDVLTSLQD-----GPYQIFLSKVKEAFQCICCOELVERP 723
QY 473 ITTVQHNVCCKDCLDRSPRAQVFCPCACRYDILGRSYAMQVNOPLQTLNQLPPGYGNGR 531
DB 724 VTTVCQHNVCCKDCLDRSPRAQVFCPCACRYDILGRSYAMQVNOPLQTLNQLPPGYGNGR 782

RESULT 6
Q6PEIO PRELIMINARY; PRT; 775 AA.
AC Q6PEIO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ubiquitin-like, containing PHD and RING finger domains, 1.
GN Name=uhrfl;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
```



```
QY 478 QHNVCKDCLDRSFRAQVFCPCACRYDLGRSYAMQVNPQLQTLVNLQFPQYGNR 531
Db 750 FHNVCCKDCLQSFKAQVFCPCACRDLGQNYVMVNLNETLQTLDLFFPGYSKGR 803

RESULT 9
Q8KI15 PRELIMINARY; PRT; 803 AA.
AC Q8KI15;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nuclear zinc finger protein Np97.
GN Names=Uhrf2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukemic cell line;
RA Davenport J.W., Fernandes E.R., Neale G.A.M., Goorha R.M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF274047; AAM33798.1; -.
DR HSSP; Q9UIG0; 1F62.
DR MGD; MGI:1923718; Uhrf2.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR011011; FYVE PHD Znf.
DR InterPro; IPR003105; SRA_YDG.
DR InterPro; IPR00626; Ubiquitin.
DR InterPro; IPR001965; Znf PHD.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00184; RING; 2.
DR SMART; SM00466; SRA; 1.
DR SMART; SM00213; UEQ; 1.
DR PROSITE; PS0053; UBIQUITIN_2; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 803 AA; 90091 MW; 99C82799305F3FA0 CRC64;

Query Match 60.7%; Score 1757.5; DB 2; Length 803;
Best Local Similarity 60.5%; Pred. No. 15e-112;
Matches 323; Conservative 74; Mismatches 112; Indels 25; Gaps 6;

QY 1 DQSLNDCRIIFVDFVKIERPGSGPM--VDNPMRRKSGPSCKHKDDVNRLCRVCAHL 58
Db 292 EGTLNDRCVMSVDEIFKIEKPG-AHPISFADGKFLKNDPECDLCGGDPDKTCHMCSCHK 350

QY 59 CGGRQDPDKQLMCDCEMAFHYICLDPPLSSVPSSEDEWCPGCRNDASEVWLAGERLRS 118
Db 351 CGEKRDNNQMLLDCENMAYHYICLSPPLDKVPEEYVPCPSCKTDSSEVWVKAERLKL 410

QY 119 KKNAKMASATSSORDWKGCMACVGTKECTIVPSNHYGPICGIPVGTWRRFRVQVSESS 178
Db 411 KKAKMPASASTERRRWGKGCMACVGTKECTIVPSNHYGPICGIPVGTWRRFRVQVSEAG 470

QY 179 VHRPHVAGIHGRSNDGSYSLVLAGGYDDVDHGNFFTYTSGGRDLISGNKRTAEQSCDQK 238
Db 750 FHNVCCKDCLQSFKAQVFCPCACRDLGQNYVMVNLNETLQTLDLFFPGYSKGR 803
```

```
Db 471 VHRPHVGGIHGRSNDGAYSLVLAGGFEDVDRGDEFTYTGSGGKNLGNKRIGAPSAQT 530
QY 239 LTNTRALALNCFAPINDQEGAEAKDWSGKVRVVRNVKGGKNSKYAPAEGRVDGIYK 298
Db 531 LTNMRALALNCDAFLDDKIGAESNRWRAGKVRVIRSPFKGRKISKYAPEEGRVDGIYK 590
QY 299 VVKYWPKEGKS-GFLVWRYLLRRDDDEPGPWTKEGDKRIKKLGLTWQYPEGVLEALANRE 357
Db 591 VVKYWPESISSHGFVWRYLLRRDDVEPAPWTSEGTIERSRRLCLRLOYPAGY-----P 643
QY 358 REKENSKEEEEQOQSGFASPTGKWKRKSGAGSPRAGSPRSTSKTKVPEYSLTAQ 417
Db 644 SEKEGKTKGQSKQSGSEATKPA-----SDDSCPGDSKVLKASDSTDAVEAFQLTQ 696
QY 418 QSSLIREDKSNAKLWNEVLASLKDRAQSPGSPQLFLSKVETFTQICCOELVFRPITTV 477
Db 697 QQLRLREDCNQKLWDEVLASLVEGPN-----FLKKLEQSFMCVCCQELVYQPVTTTC 749
QY 478 QHNVCKDCLDRSFRAQVFCPCACRYDLGRSYAMQVNPQLQTLVNLQFPQYGNR 531
Db 750 FHNVCCKDCLQSFKAQVFCPCACRDLGQNYVMVNLNETLQTLLELFFPGYSKGR 803

RESULT 10
Q96PU4 PRELIMINARY; PRT; 802 AA.
AC Q96PU4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Np95-like ring finger protein (Nuclear zinc finger protein Np97).
GN Name=NIRF; Synonyms=UHRF2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22165473; PubMed=12176013; DOI=10.1016/S0006-291X(02)00890-2;
RA Mori T., Li Y., Hata H., Ono K., Kochi H.;
RT "NIRF, a novel RING finger protein, is involved in cell-cycle regulation.";
RL Biochem. Biophys. Res. Commun. 296:530-536(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=14741369; DOI=10.1016/S0014-5793(03)01495-9;
RA Mori T., Li Y., Hata H., Kochi H.;
RT "NIRF is a ubiquitin ligase that is capable of ubiquitinating PCNP, a PEST-containing nuclear protein.";
RL FEBS Lett. 557:209-214(2004).
RN [3]
RP SEQUENCE FROM N.A.
RA Davenport J.W., Fernandes E.R., Neale G.A.M., Goorha R.M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AB071698; BAB68317.1; -.
DR EMBL; AF274049; AAM33799.1; -.
DR HSSP; Q9UIG0; 1F62.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR011011; FYVE PHD Znf.
DR InterPro; IPR00626; Ubiquitin.
DR InterPro; IPR001965; Znf PHD.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
```


Db 502 MNRALALNCSAIPINDKEGSIADKDRAGKPVVRVNRSGKHKSHYAPBEGNRVDGIYKVKV 561

QY 302 YWPEKGSGFLVWRYLLRRDDDEPGPWTKEGKDRIK 337

Db 562 YWPEKGSGFLVWRYLLRRDDDEPGPWTKEGKDKK 597

RESULT 12

Q8C6F1 PRELIMINARY; PRT; 299 AA.

AC Q8C6F1; 299 AA.

DT 01-WAR-2003 (TREMELrel. 23, Created)

DT 01-WAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)

DE Mus musculus adult male small intestine cDNA, RIKEN full-length

DE enriched library, clone:2010107E01 product:nuclear protein 95, full

DE insert sequence. (Fragment).

GN Name=Uhrfl;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN PANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Nature 420:563-573(2002).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Nature 420:563-573(2002).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [7]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [8]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [9]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [10]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [11]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [12]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [13]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [14]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [15]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Tashiro N., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,

RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-Format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,

RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK075819; BAC35985.1; -.

DR MGI; MGI:1338889; Uhrfl.

DR GO; GO:0005634; C:nucleus; TAS.

DR GO; GO:0008283; P:cell proliferation; TAS.

DR InterPro; IPR003105; SRA_YDG.

DR InterPro; IPR001841; Znf_rdg.

DR Pfam; PF02182; YDG_SRA; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.

DR PROSITE; PS00089; ZF_RING_2; 1.

KW Nuclear protein.

FT NON_TER 1

SQ SEQUENCE 299 AA; 33647 MW; 512C0893DBABF048 CRC64;

Query Match 41.7%; Score 1207; DB 2; Length 299;

Best Local Similarity 73.0%; Fred. No. 3.8e-75;

Matches 230; Conservative 35; Mismatches 34; Indels 16; Gaps 6;

QY 217 TSGGGRDLGSGNKRKTAEQSCDQKLTNNRNLALNCFAPINDOEGAEAKDWRSGKPVVRVN 276

Db 1 TSGGGRDLGSGNKRKTAEQSCDQKLTNNRNLALNCFAPINDOEGAEAKDWRSGKPVVRVN 59

QY 277 VKGKNSKYAPAEGRNRYDGIYKVPKSGFLVWRYLLRRDDDEPGPWTKEGKORI 336

Db 60 MKGKHSHKYAPAEGRNRYDGIYKVPKSGFLVWRYLLRRDDDEPGPWTKEGKORI 119

QY 337 KKLGLTMQYPEGYLEALANRREKENSKEEEOEGGFASPRTCGKWKRSAGGSPR 396

Db 120 KKLGLTMQYPEGYLEALANRREKENSKEEEOEGGFASPRTCGKWKRSAGGSPR 170

QY 397 AGSPRTSKTKTVPYSLTAQSSLIREDKSNKLVNVLASLKDPRPASGSPFLFLSKV 456

Db 171 LSSP-RASKSKLEPYLSEQANLIKEDKGNKLVNVLASLKDPRPASGSPFLFLSKV 224

QY 457 BETFOCICQELVFRPITTVQCHNVCKDCLDRSFRAQVFCPACRYDLGRSYAMOVNQL 516

Db 225 KEAFQICICQELVFRPITTVQCHNVCKDCLDRSFRAQVFCPACRYDLGRSYAMOVNQL 284

QY 517 QTVNLQPLFGYNGR 531

Db 285 QTVNLQPLFGYNGR 299

RESULT 13

Q9H6S6 PRELIMINARY; PRT; 189 AA.

AC Q9H6S6; 189 AA.

DT 01-WAR-2001 (TREMELrel. 16, Created)

DT 01-WAR-2001 (TREMELrel. 16, Last sequence update)

DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)

DE Hypothetical protein FLJ21925.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,

RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK025578; BAB15177.1; -.

DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

```
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0015567; P:protein ubiquitination; IEA.
DR InterPro: IPR001841; Znf_ring.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; UNKNOWN_1.
DR PROSITE: PS00089; ZF_RING_2; 1.
SQ SEQUENCE 189 AA; 21351 MW; 88C899C7029185AE CRC64;

Query Match
Best Local Similarity 34.7%; Score 1005; DB 2; Length 189;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 MQYPEGYLEALANRREKENSREEREEQEGGFASPRCKGKWKKSAGGGSFRAGSPRR 402
Db |||||
QY 403 TSKTKTVEPYSLTAQOSSLIREDKSNKLNWNLASLKDPRASGSPFQLFLSKVBETFOC 462
Db |||||
QY 61 TSKTKTVEPYSLTAQOSSLIREDKSNKLNWNLASLKDPRASGSPFQLFLSKVBETFOC 120
Db |||||
QY 463 ICCQELVFRPITTVCOHNVCKDCLDRSFRAQVFCPCACRYDLGRSYAMQVNPLOTLVNLQ 522
Db |||||
QY 121 ICCQELVFRPITTVCOHNVCKDCLDRSFRAQVFCPCACRYDLGRSYAMQVNPLOTLVNLQ 180
Db |||||
QY 523 LFPGYNGR 531
Db |||||
QY 181 LFPGYNGR 189

RESULT 14
Q8VIA1 PRELIMINARY; PRT; 474 AA.
AC Q8VIA1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Np95 (Fragment).
GN Name=n95;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RX MEDLINE=22206529; PubMed=12084726; DOI=10.1074/jbc.M205189200;
RA Muto M., Kanari Y., Kubo E., Takabe T., Kurihara T., Fujimori A.,
RA Tatsumi K.
RT "Targeted disruption of Np95 gene renders murine embryonic stem cells
RT hypersensitive to DNA damaging agents and DNA replication blocks.";
RL J. Biol. Chem. 277:34549-34555(2002).
DR EMBL; AB066245; BAB79496.1; -.
DR HSSP; Q9UIG0; 1F62.
DR GO: GO:000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR PRINTS; PR00348; UBIQUITIN.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE; PS00553; UBIQUITIN_2; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 53685 MW; 0EAB841CCD8C7FEA CRC64;

Query Match
30.6%; Score 886; DB 2; Length 474;

Best Local Similarity 73.5%; Pred. No. 8.5e-53;
Matches 158; Conservative 22; Mismatches 27; Indels 8; Gaps 1;

QY 1 DDLNDCRIIFVDEVFKIEREGEGSPMVDNPMR-----RKSGPSCKHCKDDVNRLCR 52
Db |||||
QY 260 DSQLNCRIMFVDEVLMIELPKERRPLIASFSQPPALRNTGKSGPSCRFCCKDDENKPCR 319
Db |||||
QY 53 VCACHLCGRQDPDKQLMCDCECDMAFHLYCLDPLSSVPSDEWYCPSCRNDASAEVVLG 112
Db |||||
QY 320 KCACHVCGRAPEKQLLCECDMAFHLYCLKPLTSVPPEPWYCPSCRTDSSESVQAG 379
Db |||||
QY 113 ERLRESKNAKMASATSSSQSDWGMGACVGRTECTIVPSNHYGPIPIGVGTWRRFRV 172
Db |||||
QY 380 EKLKESKKAKMASATSSSRDWMGMAVGRTECTIVPANHFPIPGVPVGTWRRFRV 439
Db |||||
QY 173 QVSESGVHRPHVAGIHGRSNDGYSLSVLGGYEDD 207
Db |||||
QY 440 QVSESGVHRPHVAGIPWESNDGAYSLVLGGYEDD 474
Db |||||

RESULT 15
Q8BJP6 PRELIMINARY; PRT; 516 AA.
AC Q8BJP6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length
DE enriched library, clone:B430210O11 product:hypothetical Ubiquitin
DE domain containing protein, full insert sequence.
GN Name=Uhrf2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RX MEDLINE=9273253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
```


RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK080925; BAC38081.1; -
DR HSSP; QSUIGO; IF62.
DR MGD; MGI:1923718; UmrF2.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR011011; FYVE PHD_Znf.
DR InterPro; IPR003105; SRA_YDG_Znf.
DR InterPro; IPR000626; Ubiquitin.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS50016; ZF_PHD_2; 1.
KW Hypothetical protein_
SQ SEQUENCE 516 AA; 57761 MW; 3D6862B9D1E1DEDD CRC64;

Query Match 28.2%; Score 816.5; DB 2; Length 516;
Best Local Similarity 67.1%; Pred. NO. 5.7e-48;
Matches 141; Conservative 31; Mismatches 35; Indels 3; Gaps 2;

QY 1 DDSLNDCRIFVDEVPKIERPGEQSPM--VDNPMRKSGSPCKXCKDDVNLRCVCACHL 58
DB 292 EGTLNDCRVMSVDEIFKIEKPG-AHPISFADGKFLRKNDPEDCLCGDPDKTCHMCCHK 350
QY 59 CGGRQDPDKOLMCDECMAPHIYCLDPLSSVPSDEWYCEPCRNDASEVLAGERLRES 118
DB 351 CGEKRPDPNQLLDCENMAYHIYCLSPPLDKVPFEEYCPCKTDSSEVVKAGERKLKLS 410
QY 119 KQAKMASATSSQRDWGKMACVGRKTECTIVPSNHYGPIGIPVGTWRRFRVQVSESG 178
DB 411 KKKAKMPSASTESRRDWRGRCMACVGRKTECTIVPSNHYGPIGIPVGTWRRFRVQVSEAG 470
QY 179 VHRPHVAGIHGRSNDGSYSVLVAGGYEDDV 208
DB 471 VHRPHVGGIHGRSNDGAYSILVLAGPPEDEV 500

Search completed: July 25, 2005, 17:06:45
Job time : 183 secs



THIS PAGE BLANK (USPTO)